GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 04:03:11 ; Search time 919.446 Seconds
(without alignments)
989.948 Million cell updates/sec

Title: US-09-940-860-4
Perfect score: 21
Sequence: 1 gtgccagcagcagcggtaata 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
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6: gb_pat:*
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16: em_fun:*
17: em_hum:*
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29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	410	1	AF128731	AF128731 Uncultured
2	21	100.0	420	1	AF128692	AF128692 Uncultured
3	21	100.0	434	1	AF247784	AF247784 Soil clon
4	21	100.0	440	1	AF128656	AF128656 Uncultured
5	21	100.0	495	8	AF442311	AF442311 Tetrapisi
6	21	100.0	500	1	AF280951	AF280951 Uncultured
7	21	100.0	508	1	AY193254	AY193254 Uncultured
8	21	100.0	517	1	AY193029	AY193029 Uncultured
9	21	100.0	525	1	AY193103	AY193103 Uncultured
10	21	100.0	529	3	AY293558	AY293558 Uncultured
11	21	100.0	534	8	AF442312	AF442312 Tetrapisi
12	21	100.0	550	1	AF128705	AF128705 Uncultured
13	21	100.0	552	8	AF442310	AF442310 Tetrapisi
14	21	100.0	559	1	AY037640	AY037640 Uncultured
15	21	100.0	564	1	AY193243	AY193243 Uncultured
16	21	100.0	572	1	AY037568	AY037568 Uncultured
17	21	100.0	575	1	AY037566	AY037566 Uncultured
18	21	100.0	585	1	AF432842	AF432842 Uncultured
19	21	100.0	600	8	AF442309	AF442309 Tetrapisi
20	21	100.0	620	1	AY242747	AY242747 Uncultured
21	21	100.0	620	1	AY242748	AY242748 Uncultured
22	21	100.0	621	1	AY037626	AY037626 Uncultured
23	21	100.0	648	3	AY293557	AY293557 Uncultured
24	21	100.0	650	1	AY037620	AY037620 Uncultured
25	21	100.0	670	1	AY193253	AY193253 Uncultured
26	21	100.0	702	1	AF469392	AF469392 Uncultured
27	21	100.0	756	1	AY245484	AY245484 Uncultured
28	21	100.0	766	1	AY193246	AY193246 Uncultured
29	21	100.0	771	1	AF469403	AF469403 Uncultured
30	21	100.0	784	1	AF469398	AF469398 Uncultured
31	21	100.0	796	1	AY245486	AY245486 Uncultured
32	21	100.0	824	1	AF469407	AF469407 Uncultured
33	21	100.0	935	3	PFAMTSSU	M23443 P.falciparu
34	21	100.0	939	3	AF040972	AF040972 Hepatozoo
35	21	100.0	949	3	AF040974	AF040974 Plasmodiu
36	21	100.0	956	1	GS16SJ59	X85243 Gordonia sp
37	21	100.0	961	3	AF040968	AF040968 Babesia b
38	21	100.0	991	1	AF172925	AF172925 Uncultured
39	21	100.0	991	1	AF172926	AF172926 Uncultured
40	21	100.0	991	1	AY193166	AY193166 Uncultured
41	21	100.0	995	1	AF172927	AF172927 Uncultured
42	21	100.0	998	3	AF040976	AF040976 Eimeria m
43	21	100.0	1013	3	AF040975	AF040975 Eimeria m
44	21	100.0	1023	1	AY193167	AY193167 Uncultured
45	21	100.0	1024	1	AY193190	AY193190 Uncultured

ALIGNMENTS

RESULT 1
AF128731
LOCUS AF128731 410 bp DNA linear BCT 10-MAY-1999
DEFINITION Uncultured soil bacterium C065 16S ribosomal RNA, partial sequence.
ACCESSION AF128731
VERSION AF128731.1 GI:4761945
KEYWORDS .
SOURCE uncultured soil bacterium C065
ORGANISM uncultured soil bacterium C065
Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 410)
AUTHORS Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuske,C.R.
TITLE Levels of bacterial community diversity in four arid soils compared by cultivation and 16S rRNA gene cloning
JOURNAL Appl. Environ. Microbiol. 65 (4), 1662-1669 (1999)

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  MEDLINE   99203125
   PUBMED   10103265
REFERENCE   2  (bases 1 to 410)
  AUTHORS   Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuske,C.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-FEB-1999) Environmental Molecular Biology, Life
            Sciences Division, Los Alamos National Laboratory, M888, Los
            Alamos, NM 87545, USA
FEATURES             Location/Qualifiers
     source          1. .410
                     /organism="uncultured soil bacterium C065"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:92353"
                     /clone="C065"
     rRNA            <1. .>410
                     /product="16S ribosomal RNA"
ORIGIN

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  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAATA 21
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Db        171 GTGCCAGCAGCAGCGGTAATA 191


RESULT 2
AF128692
LOCUS       AF128692                 420 bp    DNA     linear   BCT 10-MAY-1999
DEFINITION  Uncultured soil bacterium S079 16S ribosomal RNA, partial sequence.
ACCESSION   AF128692
VERSION     AF128692.1  GI:4761906
KEYWORDS    .
SOURCE      uncultured soil bacterium S079
  ORGANISM  uncultured soil bacterium S079
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 420)
  AUTHORS   Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuske,C.R.
  TITLE     Levels of bacterial community diversity in four arid soils compared
            by cultivation and 16S rRNA gene cloning
  JOURNAL   Appl. Environ. Microbiol. 65 (4), 1662-1669 (1999)
  MEDLINE   99203125
   PUBMED   10103265
REFERENCE   2  (bases 1 to 420)
  AUTHORS   Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuske,C.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-FEB-1999) Environmental Molecular Biology, Life
            Sciences Division, Los Alamos National Laboratory, M888, Los
            Alamos, NM 87545, USA
FEATURES             Location/Qualifiers
     source          1. .420
                     /organism="uncultured soil bacterium S079"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:92314"
                     /clone="S079"
     rRNA            <1. .>420
                     /product="16S ribosomal RNA"
ORIGIN

  Query Match             100.0%;  Score 21;  DB 1;  Length 420;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAATA 21
              |||||||||||||||||||||
Db        202 GTGCCAGCAGCAGCGGTAATA 222


RESULT 3
AF247784
LOCUS       AF247784                 434 bp    DNA     linear   BCT 08-SEP-2000
DEFINITION  Soil clone WD5 16S ribosomal RNA gene, partial sequence.
ACCESSION   AF247784
VERSION     AF247784.2  GI:9994208
KEYWORDS    .
SOURCE      soil clone WD5
  ORGANISM  soil clone WD5
            Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
            Sphingomonadaceae; environmental samples.
REFERENCE   1  (bases 1 to 434)
  AUTHORS   Dejonghe,W., Goris,J., El Fantroussi,S., Hofte,M., De Vos,P.,
            Verstraete,W. and Top,E.M.
  TITLE     Effect of dissemination of 2,4-dichlorophenoxyacetic acid (2,4-D)
            degradation plasmids on 2,4-D degradation and on bacterial
            community structure in two different soil horizons
  JOURNAL   Appl. Environ. Microbiol. 66 (8), 3297-3304 (2000)
  MEDLINE   20378631
   PUBMED   10919784
REFERENCE   2  (bases 1 to 434)
  AUTHORS   Dejonghe,W.L., Goris,J., El Fantroussi,S., Hofte,M., De Vos,P.,
            Verstraete,W. and Top,E.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-MAR-2000) Faculty of Agricultural and Applied
            Biological Sciences, Gent University, Coupure Links 653, Gent 9000,
            Belgium
REFERENCE   3  (bases 1 to 434)
  AUTHORS   Dejonghe,W.L., Goris,J., El Fantroussi,S., Hofte,M., De Vos,P.,
            Verstraete,W. and Top,E.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-SEP-2000) Faculty of Agricultural and Applied
            Biological Sciences, Gent University, Coupure Links 653, Gent 9000,
            Belgium
  REMARK    Sequence update by submitter
COMMENT     On Sep 8, 2000 this sequence version replaced gi:9864056.
FEATURES             Location/Qualifiers
     source          1. .434
                     /organism="soil clone WD5"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:135645"
                     /note="isolated from B-horizon at a depth of 30-60 cm"
     rRNA            <1. .>434
                     /product="16S ribosomal RNA"
ORIGIN

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  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAATA 21
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Db        413 GTGCCAGCAGCAGCGGTAATA 433


RESULT 4
AF128656
LOCUS       AF128656                 440 bp    DNA     linear   BCT 10-MAY-1999
DEFINITION  Uncultured soil bacterium C0108 16S ribosomal RNA, partial
            sequence.
ACCESSION   AF128656
VERSION     AF128656.1  GI:4761870
KEYWORDS    .
SOURCE      uncultured soil bacterium C0108
  ORGANISM  uncultured soil bacterium C0108
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 440)
  AUTHORS   Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuske,C.R.
  TITLE     Levels of bacterial community diversity in four arid soils compared
            by cultivation and 16S rRNA gene cloning
  JOURNAL   Appl. Environ. Microbiol. 65 (4), 1662-1669 (1999)
  MEDLINE   99203125
   PUBMED   10103265
REFERENCE   2  (bases 1 to 440)
  AUTHORS   Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuske,C.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-FEB-1999) Environmental Molecular Biology, Life
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            Sciences Division, Los Alamos National Laboratory, M888, Los
            Alamos, NM 87545, USA
FEATURES             Location/Qualifiers
     source          1. .440
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:92278"
                     /clone="C0108"
     rRNA            <1. .>440
                     /product="16S ribosomal RNA"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 3.7e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAATA 21
              |||||||||||||||||||||
Db        200 GTGCCAGCAGCAGCGGTAATA 220


RESULT 5
AF442311
LOCUS       AF442311                 495 bp    DNA     linear   PLN 11-JUN-2003
DEFINITION  Tetrapisispora arboricola small subunit ribosomal RNA gene, partial
            sequence; mitochondrial gene for mitochondrial product.
ACCESSION   AF442311
VERSION     AF442311.1  GI:31581325
KEYWORDS    .
SOURCE      mitochondrion Tetrapisispora arboricola
  ORGANISM  Tetrapisispora arboricola
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Tetrapisispora.
REFERENCE   1  (bases 1 to 495)
  AUTHORS   Kurtzman,C.P. and Robnett,C.J.
  TITLE     Phylogenetic relationships among yeasts of the 'Saccharomyces
            complex' determined from multigene sequence analyses
  JOURNAL   FEMS Yeast Res. 3 (4), 417-432 (2003)
  MEDLINE   22633405
   PUBMED   12748053
REFERENCE   2  (bases 1 to 495)
  AUTHORS   Kurtzman,C.P. and Robnett,C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-NOV-2001) United States Department of Agriculture,
            National Center for Agricultural Utilization Research, 1815 N.
            University St., Peoria, IL 61604, USA
FEATURES             Location/Qualifiers
     source          1. .495
                     /organism="Tetrapisispora arboricola"
                     /organelle="mitochondrion"
                     /mol_type="genomic DNA"
                     /strain="NRRL Y-27308"
                     /db_xref="taxon:113605"
                     /clone="A314"
     rRNA            <1. .>495
                     /product="small subunit ribosomal RNA"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAATA 21
              |||||||||||||||||||||
Db        114 GTGCCAGCAGCAGCGGTAATA 134


RESULT 6
AF280951
LOCUS       AF280951                 500 bp    DNA     linear   BCT 09-JUL-2001
DEFINITION  Uncultured bacterium clone JS11 16S ribosomal RNA gene, partial
            sequence.
ACCESSION   AF280951
VERSION     AF280951.1  GI:9255904
KEYWORDS    .
SOURCE      uncultured bacterium
  ORGANISM  uncultured bacterium
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 500)
  AUTHORS   Stach,J.E., Bathe,S., Clapp,J.P. and Burns,R.G.
  TITLE     PCR-SSCP comparison of 16S rDNA sequence diversity in soil DNA
            obtained using different isolation and purification methods
  JOURNAL   FEMS Microbiol. Ecol. 36 (2-3), 139-151 (2001)
   PUBMED   11451518
REFERENCE   2  (bases 1 to 500)
  AUTHORS   Stach,J.E., Bathe,S. and Burns,R.G.
  TITLE     Evaluation and Optimization of DNA extraction and Purification from
            soil by Single-Strand-Conformation Polymorphism
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 500)
  AUTHORS   Stach,J.E., Bathe,S. and Burns,R.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUN-2000) Biosciences, University of Kent at
            Canterbury, University Rd, Canterbury, Kent CT2 7NJ, England
FEATURES             Location/Qualifiers
     source          1. .500
                     /organism="uncultured bacterium"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:77133"
                     /clone="JS11"
                     /note="environmental clone"
     rRNA            <1. .>500
                     /product="16S ribosomal RNA"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAATA 21
              |||||||||||||||||||||
Db        135 GTGCCAGCAGCAGCGGTAATA 155


RESULT 7
AY193254
LOCUS       AY193254                 508 bp    DNA     linear   BCT 19-FEB-2003
DEFINITION  Uncultured bacterium clone Bol64 16S ribosomal RNA gene, partial
            sequence.
ACCESSION   AY193254
VERSION     AY193254.1  GI:28436012
KEYWORDS    .
SOURCE      uncultured bacterium
  ORGANISM  uncultured bacterium
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 508)
  AUTHORS   Harris,J.Kirk., Kelley,S.T. and Pace,N.R.
  TITLE     New perspective on uncultured bacterial phylogenetic division OP11
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 508)
  AUTHORS   Harris,J.Kirk., Kelley,S.T. and Pace,N.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2002) Molecular, Cellular and Developmental
            Biology, University of Colorado, Campus box 347, Boulder, CO 80309,
            USA
FEATURES             Location/Qualifiers
     source          1. .508
                     /organism="uncultured bacterium"
                     /mol_type="genomic DNA"
                     /isolation_source="marine sediment"
                     /db_xref="taxon:77133"
                     /clone="Bol64"
                     /environmental_sample
     rRNA            <1. .>508
                     /product="16S ribosomal RNA"
ORIGIN
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  Query Match             100.0%;  Score 21;  DB 1;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAATA 21
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Db        430 GTGCCAGCAGCAGCGGTAATA 450


RESULT 8
AY193029
LOCUS       AY193029                517 bp    DNA     linear   BCT 19-FEB-2003
DEFINITION  Uncultured candidate division OP11 bacterium clone WSA86 16S
            ribosomal RNA gene, partial sequence.
ACCESSION   AY193029
VERSION     AY193029.1  GI:28435787
KEYWORDS    .
SOURCE      uncultured candidate division OP11 bacterium
  ORGANISM  uncultured candidate division OP11 bacterium
            Bacteria; candidate division OP11; environmental samples.
REFERENCE   1  (bases 1 to 517)
  AUTHORS   Harris,J.Kirk., Kelley,S.T. and Pace,N.R.
  TITLE     New perspective on uncultured bacterial phylogenetic division OP11
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 517)
  AUTHORS   Harris,J.Kirk., Kelley,S.T. and Pace,N.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2002) Molecular, Cellular and Developmental
            Biology, University of Colorado, Campus box 347, Boulder, CO 80309,
            USA
FEATURES             Location/Qualifiers
     source          1. .517
                     /organism="uncultured candidate division OP11 bacterium"
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                     /isolation_source="contaminated aquifer"
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                     /clone="WSA86"
                     /environmental_sample
     rRNA            <1. .>517
                     /product="16S ribosomal RNA"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAATA 21
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Db        433 GTGCCAGCAGCAGCGGTAATA 453


RESULT 9
AY193103
LOCUS       AY193103                525 bp    DNA     linear   BCT 19-FEB-2003
DEFINITION  Uncultured bacterium clone DA43 16S ribosomal RNA gene, partial
            sequence.
ACCESSION   AY193103
VERSION     AY193103.1  GI:28435861
KEYWORDS    .
SOURCE      uncultured bacterium
  ORGANISM  uncultured bacterium
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 525)
  AUTHORS   Harris,J.Kirk., Kelley,S.T. and Pace,N.R.
  TITLE     New perspective on uncultured bacterial phylogenetic division OP11
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 525)
  AUTHORS   Harris,J.Kirk., Kelley,S.T. and Pace,N.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2002) Molecular, Cellular and Developmental
            Biology, University of Colorado, Campus box 347, Boulder, CO 80309,
            USA
FEATURES             Location/Qualifiers
     source          1. .525
                     /organism="uncultured bacterium"
                     /mol_type="genomic DNA"
                     /isolation_source="contaminated aquifer"
                     /db_xref="taxon:77133"
                     /clone="DA43"
                     /environmental_sample
     rRNA            <1. .>525
                     /product="16S ribosomal RNA"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAATA 21
              |||||||||||||||||||||
Db        431 GTGCCAGCAGCAGCGGTAATA 451


RESULT 10
AY293558
LOCUS       AY293558                529 bp    DNA     linear   INV 05-JUN-2003
DEFINITION  Uncultured phototrophic eukaryote clone FL14G11 16S ribosomal RNA
            gene, partial sequence; chloroplast gene for chloroplast product.
ACCESSION   AY293558
VERSION     AY293558.1  GI:31416275
KEYWORDS    .
SOURCE      chloroplast uncultured phototrophic eukaryote
  ORGANISM  uncultured phototrophic eukaryote
            Eukaryota; environmental samples.
REFERENCE   1  (bases 1 to 529)
  AUTHORS   Bonheyo,G.T., Fouke,B.W., Martin,H.G., Veysey,J., Goldenfeld,N. and
            Frias-Lopez,J.
  TITLE     Partitioning of Mineralogical, Geochemical, and Microbial Systems
            in Travertine Terraces at Yellowstone Hot Springs
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 529)
  AUTHORS   Bonheyo,G.T., Fouke,B.W., Martin,H.G., Veysey,J., Goldenfeld,N. and
            Frias-Lopez,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAY-2003) Geology, University of Illinois, 245
            Natural History Building, 1301 West Green St, Urbana, IL 61801, USA
FEATURES             Location/Qualifiers
     source          1. .529
                     /organism="uncultured phototrophic eukaryote"
                     /organelle="plastid:chloroplast"
                     /mol_type="genomic DNA"
                     /isolation_source="travertine terrace, Yellowstone Hot
                     Springs"
                     /db_xref="taxon:172788"
                     /clone="FL14G11"
                     /environmental_sample
     rRNA            <1. .>529
                     /product="16S ribosomal RNA"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAATA 21
              |||||||||||||||||||||
Db        468 GTGCCAGCAGCAGCGGTAATA 488


RESULT 11
AF442312
LOCUS       AF442312                534 bp    DNA     linear   PLN 11-JUN-2003
DEFINITION  Tetrapisispora iriomotensis small subunit ribosomal RNA gene,
            partial sequence; mitochondrial gene for mitochondrial product.
ACCESSION   AF442312
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VERSION     AF442312.1  GI:31581326
KEYWORDS    .
SOURCE      mitochondrion Tetrapisispora iriomotensis
  ORGANISM  Tetrapisispora iriomotensis
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Tetrapisispora.
REFERENCE   1  (bases 1 to 534)
  AUTHORS   Kurtzman,C.P. and Robnett,C.J.
  TITLE     Phylogenetic relationships among yeasts of the 'Saccharomyces
            complex' determined from multigene sequence analyses
  JOURNAL   FEMS Yeast Res. 3 (4), 417-432 (2003)
  MEDLINE   22633405
   PUBMED   12748053
REFERENCE   2  (bases 1 to 534)
  AUTHORS   Kurtzman,C.P. and Robnett,C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-NOV-2001) United States Department of Agriculture,
            National Center for Agricultural Utilization Research, 1815 N.
            University St., Peoria, IL 61604, USA
FEATURES             Location/Qualifiers
     source          1. .534
                     /organism="Tetrapisispora iriomotensis"
                     /organelle="mitochondrion"
                     /mol_type="genomic DNA"
                     /strain="NRRL Y-27309"
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                     /clone="A315"
     rRNA            <1. .>534
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ORIGIN

  Query Match             100.0%;  Score 21;  DB 8;  Length 534;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAATA 21
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Db        154 GTGCCAGCAGCAGCGGTAATA 174


RESULT 12
AF128705
LOCUS       AF128705                550 bp    DNA     linear   BCT 10-MAY-1999
DEFINITION  Uncultured soil bacterium S0212 16S ribosomal RNA, partial
            sequence.
ACCESSION   AF128705
VERSION     AF128705.1  GI:4761919
KEYWORDS    .
SOURCE      uncultured soil bacterium S0212
  ORGANISM  uncultured soil bacterium S0212
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 550)
  AUTHORS   Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuske,C.R.
  TITLE     Levels of bacterial community diversity in four arid soils compared
            by cultivation and 16S rRNA gene cloning
  JOURNAL   Appl. Environ. Microbiol. 65 (4), 1662-1669 (1999)
  MEDLINE   99203125
   PUBMED   10103265
REFERENCE   2  (bases 1 to 550)
  AUTHORS   Dunbar,J., Takala,S., Barns,S.M., Davis,J.A. and Kuske,C.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-FEB-1999) Environmental Molecular Biology, Life
            Sciences Division, Los Alamos National Laboratory, M888, Los
            Alamos, NM 87545, USA
FEATURES             Location/Qualifiers
     source          1. .550
                     /organism="uncultured soil bacterium S0212"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:92327"
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     rRNA            <1. .>550
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ORIGIN

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  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAATA 21
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Db        297 GTGCCAGCAGCAGCGGTAATA 317


RESULT 13
AF442310
LOCUS       AF442310                552 bp    DNA     linear   PLN 11-JUN-2003
DEFINITION  Tetrapisispora nanseiensis small subunit ribosomal RNA gene,
            partial sequence; mitochondrial gene for mitochondrial product.
ACCESSION   AF442310
VERSION     AF442310.1  GI:31581324
KEYWORDS    .
SOURCE      mitochondrion Tetrapisispora nanseiensis
  ORGANISM  Tetrapisispora nanseiensis
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Tetrapisispora.
REFERENCE   1  (bases 1 to 552)
  AUTHORS   Kurtzman,C.P. and Robnett,C.J.
  TITLE     Phylogenetic relationships among yeasts of the 'Saccharomyces
            complex' determined from multigene sequence analyses
  JOURNAL   FEMS Yeast Res. 3 (4), 417-432 (2003)
  MEDLINE   22633405
   PUBMED   12748053
REFERENCE   2  (bases 1 to 552)
  AUTHORS   Kurtzman,C.P. and Robnett,C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-NOV-2001) United States Department of Agriculture,
            National Center for Agricultural Utilization Research, 1815 N.
            University St., Peoria, IL 61604, USA
FEATURES             Location/Qualifiers
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                     /organism="Tetrapisispora nanseiensis"
                     /organelle="mitochondrion"
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                     /strain="NRRL Y-27310"
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                     /clone="A316"
     rRNA            <1. .>552
                     /product="small subunit ribosomal RNA"
ORIGIN

  Query Match             100.0%;  Score 21;  DB 8;  Length 552;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAATA 21
              |||||||||||||||||||||
Db        177 GTGCCAGCAGCAGCGGTAATA 197


RESULT 14
AY037640
LOCUS       AY037640                559 bp    DNA     linear   BCT 05-MAR-2002
DEFINITION  Uncultured soil bacterium clone S133 16S ribosomal RNA gene,
            partial sequence.
ACCESSION   AY037640
VERSION     AY037640.1  GI:15789072
KEYWORDS    .
SOURCE      uncultured soil bacterium
  ORGANISM  uncultured soil bacterium
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 559)
  AUTHORS   Furlong,M.A., Singleton,D.R., Coleman,D.C. and Whitman,W.B.
  TITLE     Molecular and culture-based analyses of prokaryotic communities
            from an agricultural soil and the burrows and casts of the
            earthworm Lumbricus rubellus
  JOURNAL   Appl. Environ. Microbiol. 68 (3), 1265-1279 (2002)
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  MEDLINE   21861246
   PUBMED   11872477
REFERENCE   2  (bases 1 to 559)
  AUTHORS   Singleton,D.R., Furlong,M.A., Coleman,D.C. and Whitman,W.B.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAY-2001) Department of Microbiology, University of
            Georgia, 541 Biological Sciences Bldg, Athens, GA 30602-2605, USA
FEATURES             Location/Qualifiers
     source          1. .559
                     /organism="uncultured soil bacterium"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:164851"
                     /clone="S133"
     rRNA            <1. .>559
                     /product="16S ribosomal RNA"
ORIGIN

  Query Match             100.0%;  Score 21;  DB 1;  Length 559;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAATA 21
              |||||||||||||||||||||
Db        411 GTGCCAGCAGCAGCGGTAATA 431


RESULT 15
AY193243
LOCUS       AY193243                 564 bp    DNA     linear   BCT 19-FEB-2003
DEFINITION  Uncultured bacterium clone Bol43 16S ribosomal RNA gene, partial
            sequence.
ACCESSION   AY193243
VERSION     AY193243.1  GI:28436001
KEYWORDS    .
SOURCE      uncultured bacterium
  ORGANISM  uncultured bacterium
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 564)
  AUTHORS   Harris,J.Kirk., Kelley,S.T. and Pace,N.R.
  TITLE     New perspective on uncultured bacterial phylogenetic division OP11
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 564)
  AUTHORS   Harris,J.Kirk., Kelley,S.T. and Pace,N.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2002) Molecular, Cellular and Developmental
            Biology, University of Colorado, Campus box 347, Boulder, CO 80309,
            USA
FEATURES             Location/Qualifiers
     source          1. .564
                     /organism="uncultured bacterium"
                     /mol_type="genomic DNA"
                     /isolation_source="marine sediment"
                     /db_xref="taxon:77133"
                     /clone="Bol43"
                     /environmental_sample
     rRNA            <1. .>564
                     /product="16S ribosomal RNA"
ORIGIN

  Query Match             100.0%;  Score 21;  DB 1;  Length 564;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAATA 21
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 06:01:54 ; Search time 36.1446 Seconds
(without alignments)
307.073 Million cell updates/sec

Title: US-09-940-860-1
Perfect score: 20
Sequence: 1 gcaaacaggattagataccc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

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Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	24	3	US-09-073-465-9	Sequence 9, Appli
c 2	20	100.0	195	1	US-08-227-475-7	Sequence 7, Appli
c 3	20	100.0	279	4	US-09-107-532A-3170	Sequence 3170, Ap
c 4	20	100.0	279	4	US-09-107-532A-3171	Sequence 3171, Ap
5	20	100.0	538	3	US-08-979-586-3	Sequence 3, Appli
6	20	100.0	538	4	US-09-577-640-3	Sequence 3, Appli
7	20	100.0	571	3	US-09-328-111-755	Sequence 755, App
8	20	100.0	619	3	US-08-953-171-2	Sequence 2, Appli
c 9	20	100.0	624	3	US-09-328-111-728	Sequence 728, App
10	20	100.0	660	1	US-08-114-695A-5	Sequence 5, Appli
11	20	100.0	665	3	US-09-328-111-476	Sequence 476, App
12	20	100.0	672	3	US-09-328-111-450	Sequence 450, App
13	20	100.0	851	1	US-07-898-905-1	Sequence 1, Appli
14	20	100.0	851	1	US-07-898-905-2	Sequence 2, Appli
15	20	100.0	851	1	US-07-898-905-3	Sequence 3, Appli
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17	20	100.0	851	3	US-09-006-089-2	Sequence 2, Appli
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19	20	100.0	876	2	US-08-642-229A-4	Sequence 4, Appli
20	20	100.0	881	5	PCT-US91-01574-13	Sequence 13, Appl
21	20	100.0	882	2	US-07-923-871C-13	Sequence 13, Appl
22	20	100.0	1208	3	US-09-187-946-1	Sequence 1, Appli
23	20	100.0	1325	2	US-08-632-470-50	Sequence 50, Appl
24	20	100.0	1336	2	US-08-437-013-3	Sequence 3, Appli
25	20	100.0	1336	4	US-09-275-506A-3	Sequence 3, Appli
26	20	100.0	1366	3	US-09-191-099-4	Sequence 4, Appli
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30	20	100.0	1405	3	US-09-191-099-5	Sequence 5, Appli
31	20	100.0	1407	3	US-09-193-377B-2	Sequence 2, Appli
32	20	100.0	1407	4	US-09-517-744B-1	Sequence 1, Appli
33	20	100.0	1408	2	US-08-632-470-40	Sequence 40, Appl
34	20	100.0	1413	3	US-09-191-099-1	Sequence 1, Appli
35	20	100.0	1414	3	US-09-191-099-6	Sequence 6, Appli
36	20	100.0	1415	2	US-08-632-470-52	Sequence 52, Appl
37	20	100.0	1415	3	US-09-193-377B-9	Sequence 9, Appli
38	20	100.0	1417	3	US-09-191-099-2	Sequence 2, Appli
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41	20	100.0	1420	3	US-09-193-377B-4	Sequence 4, Appli
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43	20	100.0	1427	2	US-08-632-470-27	Sequence 27, Appl
44	20	100.0	1428	3	US-09-193-377B-1	Sequence 1, Appli
45	20	100.0	1429	3	US-09-193-377B-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-073-465-9
; Sequence 9, Application US/09073465
; Patent No. 6054278
; GENERAL INFORMATION:
; APPLICANT: DODGE, Deborah E
; APPLICANT: SMITH, Doug
; TITLE OF INVENTION: RIBOSOMAL RNA GENE POLYMORPHISM BASED MICROORGANISM
; TITLE OF INVENTION: IDENTIFICATION
; FILE REFERENCE: 4343 US
; CURRENT APPLICATION NUMBER: US/09/073,465
; CURRENT FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Bacterial
US-09-073-465-9

Query Match 100.0%; Score 20; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
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Db 2 GCAAACAGGATTAGATACCC 21

RESULT 2
US-08-227-475-7/c
; Sequence 7, Application US/08227475
; Patent No. 5571674
; GENERAL INFORMATION:
; APPLICANT: Hoshina, Sadayori
; APPLICANT: Weinstein, I. Bernard
; TITLE OF INVENTION: DNA Oligomers For Use In Detection Of
; TITLE OF INVENTION: Microorganisms And Methods Of Using Such DNA
; TITLE OF INVENTION: Oligomers
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:

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;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.24
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/227,475
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/672,691
;       FILING DATE:  18-MAR-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  White, John P.
;       REGISTRATION NUMBER:  28,678
;       REFERENCE/DOCKET NUMBER:  34546-A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 977-9550
;       TELEFAX:  (212) 664-0525
;       TELEX:  (212) 422523 COOP UI
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  195 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  DNA (genomic)
;     HYPOTHETICAL:  N
;     ANTI-SENSE:  N
US-08-227-475-7

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  Best Local Similarity   100.0%;  Pred. No. 0.014;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        128 GCAAACAGGATTAGATACCC 109


RESULT 3
US-09-107-532A-3170/c
; Sequence 3170, Application US/09107532A
; Patent No. 6583275
;   GENERAL INFORMATION:
;       APPLICANT: Lynn A Doucette-Stamm  and David Bush
;       TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                           ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;       NUMBER OF SEQUENCES: 7310
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;            STREET: 100 Beaver Street
;            CITY: Waltham
;            STATE: Massachusetts
;            COUNTRY: USA
;            ZIP: 02354
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD/ROM ISO9660
;            COMPUTER: PC
;            OPERATING SYSTEM: <Unknown>
;            SOFTWARE: ASCII
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/107,532A
;            FILING DATE: 30-Jun-1998
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/085,598
;            FILING DATE: 14 May 1998
;            APPLICATION NUMBER: 60/051571
;            FILING DATE: July 2, 1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ariniello, Pamela Deneke
;            REGISTRATION NUMBER: 40,489
;            REFERENCE/DOCKET NUMBER: GTC-012
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (781)893-5007
;            TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 3170:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 279 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: circular
;       MOLECULE TYPE: DNA (genomic)
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       ORIGINAL SOURCE:
;            ORGANISM: Enterococcus faecium
;       FEATURE:
;            NAME/KEY:  misc_feature
;            LOCATION: (B) LOCATION 1...279
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3170:
US-09-107-532A-3170

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  Best Local Similarity   100.0%;  Pred. No. 0.014;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        134 GCAAACAGGATTAGATACCC 115


RESULT 4
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; Sequence 3171, Application US/09107532A
; Patent No. 6583275
;   GENERAL INFORMATION:
;       APPLICANT: Lynn A Doucette-Stamm  and David Bush
;       TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                           ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;       NUMBER OF SEQUENCES: 7310
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;            STREET: 100 Beaver Street
;            CITY: Waltham
;            STATE: Massachusetts
;            COUNTRY: USA
;            ZIP: 02354
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD/ROM ISO9660
;            COMPUTER: PC
;            OPERATING SYSTEM: <Unknown>
;            SOFTWARE: ASCII
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/107,532A
;            FILING DATE: 30-Jun-1998
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/085,598
;            FILING DATE: 14 May 1998
;            APPLICATION NUMBER: 60/051571
;            FILING DATE: July 2, 1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ariniello, Pamela Deneke
;            REGISTRATION NUMBER: 40,489
;            REFERENCE/DOCKET NUMBER: GTC-012
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (781)893-5007
;            TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 3171:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 279 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: circular
;       MOLECULE TYPE: DNA (genomic)
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
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;            ORGANISM: Enterococcus faecium
;       FEATURE:
;            NAME/KEY:  misc_feature
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US-09-107-532A-3171

  Query Match             100.0%;  Score 20;  DB 4;  Length 279;
  Best Local Similarity   100.0%;  Pred. No. 0.014;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
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Db        134 GCAAACAGGATTAGATACCC 115


RESULT 5
US-08-979-586-3
; Sequence 3, Application US/08979586
; Patent No. 6190903
;  GENERAL INFORMATION:
;    APPLICANT:  Weinstein, I. B., et al.
;    TITLE OF INVENTION:  BACTERIUM CAPABLE OF BIODEGRADATION OF WASTES
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/979,586
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  52208/JPW/JKM
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-278-0400
;      TELEFAX:  212-391-0526
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  538 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-979-586-3

  Query Match             100.0%;  Score 20;  DB 3;  Length 538;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
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Db        234 GCAAACAGGATTAGATACCC 253


RESULT 6
US-09-577-640-3
; Sequence 3, Application US/09577640
; Patent No. 6420165
; GENERAL INFORMATION:
;  APPLICANT:  The Trustees of Columbia University in the City of
;  TITLE OF INVENTION:  Bacterium Capable of Biodegradation of Wastes
;  FILE REFERENCE:  52208apct
;  CURRENT APPLICATION NUMBER: US/09/577,640
;  CURRENT FILING DATE:  2000-05-24
;  PRIOR APPLICATION NUMBER:  08/979,586
;  PRIOR FILING DATE:  1997-11-26
;  NUMBER OF SEQ ID NOS:  3
;  SOFTWARE:  PatentIn Ver. 2.0 - beta
; SEQ ID NO 3
;   LENGTH: 538
;   TYPE: DNA
;   ORGANISM: Bacillus midousuji
US-09-577-640-3

  Query Match             100.0%;  Score 20;  DB 4;  Length 538;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db        234 GCAAACAGGATTAGATACCC 253


RESULT 7
US-09-328-111-755
; Sequence 755, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
;  APPLICANT: Endege, Wilson O.
;  APPLICANT: Steinmann, Kathleen E.
;  APPLICANT: Astle, Jon H.
;  APPLICANT: Burgess, Christopher C.
;  APPLICANT: Bushnell, Steven E.
;  APPLICANT: Carroll III, Eddie
;  APPLICANT: Catino, Theodore J.
;  APPLICANT: Derti, Adnan
;  APPLICANT: Ford, Donna M.
;  APPLICANT: Lewis, Marcia E.
;  APPLICANT: Monahan, John E.
;  APPLICANT: Schlegel, Robert
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
;  TITLE OF INVENTION: PRODUCTS
;  FILE REFERENCE: CCD-257 (US)
;  CURRENT APPLICATION NUMBER: US/09/328,111
;  CURRENT FILING DATE: 1999-06-08
;  EARLIER APPLICATION NUMBER: US 60/088,801
;  EARLIER FILING DATE: 1998-06-10
;  NUMBER OF SEQ ID NOS: 850
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 755
;   LENGTH: 571
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(571)
;   OTHER INFORMATION: n = A,T,C or G
US-09-328-111-755

  Query Match             100.0%;  Score 20;  DB 3;  Length 571;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db        295 GCAAACAGGATTAGATACCC 314


RESULT 8
US-08-953-171-2
; Sequence 2, Application US/08953171
; Patent No. 6124094
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;  GENERAL INFORMATION:
;    APPLICANT:  LAJOIE, CURTIS
;    APPLICANT:  LAYTON, ALICE
;    APPLICANT:  KELLY, CHIRSTINE
;    APPLICANT:  SAYLER, GARY
;    APPLICANT:  STAPLETON, RAYMOND
;    TITLE OF INVENTION:  ZOOGLOEAL AND HYPHOMICROBIUM
;    TITLE OF INVENTION:  SPP. NUCLEIC ACIDS
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NEEDLE & ROSENBERG, P.C.
;      STREET:  127 Peachtree Street, N.E., Suite 1200
;      CITY:  Atlanta
;      STATE:  GA
;      COUNTRY:  USA
;      ZIP:  30303-1811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/953,171
;      FILING DATE:  17-OCT-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Spratt, Gwendolyn DD
;      REGISTRATION NUMBER:  36,016
;      REFERENCE/DOCKET NUMBER:  05015.018
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404 688 0770
;      TELEFAX:  404 688 9880
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  619 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-953-171-2

  Query Match             100.0%;  Score 20;  DB 3;  Length 619;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db        241 GCAAACAGGATTAGATACCC 260


RESULT 9
US-09-328-111-728/c
; Sequence 728, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
;  APPLICANT: Endege, Wilson O.
;  APPLICANT: Steinmann, Kathleen E.
;  APPLICANT: Astle, Jon H.
;  APPLICANT: Burgess, Christopher C.
;  APPLICANT: Bushnell, Steven E.
;  APPLICANT: Carroll III, Eddie
;  APPLICANT: Catino, Theodore J.
;  APPLICANT: Derti, Adnan
;  APPLICANT: Ford, Donna M.
;  APPLICANT: Lewis, Marcia E.
;  APPLICANT: Monahan, John E.
;  APPLICANT: Schlegel, Robert
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
;  TITLE OF INVENTION: PRODUCTS
;  FILE REFERENCE: CCD-257 (US)
;  CURRENT APPLICATION NUMBER: US/09/328,111
;  CURRENT FILING DATE: 1999-06-08
;  EARLIER APPLICATION NUMBER: US 60/088,801
;  EARLIER FILING DATE: 1998-06-10
;  NUMBER OF SEQ ID NOS: 850
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 728
;   LENGTH: 624
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(624)
;   OTHER INFORMATION: n = A,T,C or G
US-09-328-111-728

  Query Match             100.0%;  Score 20;  DB 3;  Length 624;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db        383 GCAAACAGGATTAGATACCC 364


RESULT 10
US-08-114-695A-5
; Sequence 5, Application US/08114695A
; Patent No. 5508193
;  GENERAL INFORMATION:
;    APPLICANT:  Mandelbaum, Raphael T.
;    APPLICANT:  Wackett, Lawrence P.
;    TITLE OF INVENTION:  DEGRADATION OF S-TRIAZINES IN SOIL AND
;    TITLE OF INVENTION:  WATER
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCHWEGMAN, LUNDBERG & WOESSNER, P.A.
;      STREET:  3500 IDS CENTER
;      CITY:  MINNEAPOLIS
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/114,695A
;      FILING DATE:  31-AUG-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MUETING, ANN M.
;      REGISTRATION NUMBER:  33,977
;      REFERENCE/DOCKET NUMBER:  600.268US1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-339-0331
;      TELEFAX:  612-339-3061
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  660 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  rRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Pseudomonas citronellolis
US-08-114-695A-5

  Query Match             100.0%;  Score 20;  DB 1;  Length 660;
  Best Local Similarity   85.0%;  Pred. No. 0.013;
  Matches   17;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||::|||:||||
Db         50 GCAAACAGGAUUAGAUACCC 69


RESULT 11
US-09-328-111-476
; Sequence 476, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
;  APPLICANT: Endege, Wilson O.
;  APPLICANT: Steinmann, Kathleen E.
;  APPLICANT: Astle, Jon H.
;  APPLICANT: Burgess, Christopher C.
;  APPLICANT: Bushnell, Steven E.
;  APPLICANT: Carroll III, Eddie
;  APPLICANT: Catino, Theodore J.
;  APPLICANT: Derti, Adnan
;  APPLICANT: Ford, Donna M.
;  APPLICANT: Lewis, Marcia E.
;  APPLICANT: Monahan, John E.
;  APPLICANT: Schlegel, Robert
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
;  TITLE OF INVENTION: PRODUCTS
;  FILE REFERENCE: CCD-257 (US)
;  CURRENT APPLICATION NUMBER: US/09/328,111
;  CURRENT FILING DATE: 1999-06-08
;  EARLIER APPLICATION NUMBER: US 60/088,801
;  EARLIER FILING DATE: 1998-06-10
;  NUMBER OF SEQ ID NOS: 850
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 476
;   LENGTH: 665
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(665)
;   OTHER INFORMATION: n = A,T,C or G
US-09-328-111-476

  Query Match           100.0%;  Score 20;  DB 3;  Length 665;
  Best Local Similarity  100.0%;  Pred. No. 0.013;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db        292 GCAAACAGGATTAGATACCC 311


RESULT 12
US-09-328-111-450
; Sequence 450, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
;  APPLICANT: Endege, Wilson O.
;  APPLICANT: Steinmann, Kathleen E.
;  APPLICANT: Astle, Jon H.
;  APPLICANT: Burgess, Christopher C.
;  APPLICANT: Bushnell, Steven E.
;  APPLICANT: Carroll III, Eddie
;  APPLICANT: Catino, Theodore J.
;  APPLICANT: Derti, Adnan
;  APPLICANT: Ford, Donna M.
;  APPLICANT: Lewis, Marcia E.
;  APPLICANT: Monahan, John E.
;  APPLICANT: Schlegel, Robert
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
;  TITLE OF INVENTION: PRODUCTS
;  FILE REFERENCE: CCD-257 (US)
;  CURRENT APPLICATION NUMBER: US/09/328,111
;  CURRENT FILING DATE: 1999-06-08
;  EARLIER APPLICATION NUMBER: US 60/088,801
;  EARLIER FILING DATE: 1998-06-10
;  NUMBER OF SEQ ID NOS: 850
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 450
;   LENGTH: 672
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-328-111-450

  Query Match           100.0%;  Score 20;  DB 3;  Length 672;
  Best Local Similarity  100.0%;  Pred. No. 0.013;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db        292 GCAAACAGGATTAGATACCC 311


RESULT 13
US-07-898-905-1
; Sequence 1, Application US/07898905
; Patent No. 5424187
;  GENERAL INFORMATION:
;    APPLICANT:  Shor;Kuo
;    TITLE OF INVENTION:  "DIAGNOSIS AND TREATMENT OF ARTERIAL
;    TITLE OF INVENTION:  CHLAMYDIAL GRANULOMA"
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Christensen, O'Connor, Johnson and Kindness
;      STREET:  2800 Pacific First Center, 1420 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98101-2347
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette-5.25 inch, 1.2Mb storage
;      COMPUTER:  IBM PC/386 Compatible
;      OPERATING SYSTEM:  MS-DOS 4.01
;      SOFTWARE:  Word for Windows-t
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/898,905
;      FILING DATE:  19920612
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  none
;      FILING DATE:  none
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sundsmo,John,S.
;      REGISTRATION NUMBER:  34,446
;      REFERENCE/DOCKET NUMBER:  UOFW-1-6521
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  1-206-682-8100; 1-206-224-0727 (direct)
;      TELEFAX:  1-206-224-0779
;      TELEX:  4938023
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  851 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;      DESCRIPTION:  Case 7
US-07-898-905-1

  Query Match           100.0%;  Score 20;  DB 1;  Length 851;
  Best Local Similarity  100.0%;  Pred. No. 0.012;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db        610 GCAAACAGGATTAGATACCC 629
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```
RESULT 14
US-07-898-905-2
; Sequence 2, Application US/07898905
; Patent No. 5424187
;  GENERAL INFORMATION:
;    APPLICANT:  Shor;Kuo
;    TITLE OF INVENTION:  "DIAGNOSIS AND TREATMENT OF ARTERIAL
;    TITLE OF INVENTION:  CHLAMYDIAL GRANULOMA"
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Christensen, O'Connor, Johnson and Kindness
;      STREET:  2800 Pacific First Center, 1420 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98101-2347
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette-5.25 inch, 1.2Mb storage
;      COMPUTER:  IBM PC/386 Compatible
;      OPERATING SYSTEM:  MS-DOS 4.01
;      SOFTWARE:  Word for Windows-t
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/898,905
;      FILING DATE:  19920612
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  none
;      FILING DATE:  none
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sundsmo,John,S.
;      REGISTRATION NUMBER:  34,446
;      REFERENCE/DOCKET NUMBER:  UOFW-1-6521
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  1-206-682-8100; 1-206-224-0727 (direct)
;      TELEFAX:  1-206-224-0779
;      TELEX:  4938023
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  851 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;      DESCRIPTION:  Cpn
US-07-898-905-2

  Query Match           100.0%;  Score 20;  DB 1;  Length 851;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db        610 GCAAACAGGATTAGATACCC 629


RESULT 15
US-07-898-905-3
; Sequence 3, Application US/07898905
; Patent No. 5424187
;  GENERAL INFORMATION:
;    APPLICANT:  Shor;Kuo
;    TITLE OF INVENTION:  "DIAGNOSIS AND TREATMENT OF ARTERIAL
;    TITLE OF INVENTION:  CHLAMYDIAL GRANULOMA"
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Christensen, O'Connor, Johnson and Kindness
;      STREET:  2800 Pacific First Center, 1420 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98101-2347
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette-5.25 inch, 1.2Mb storage
;      COMPUTER:  IBM PC/386 Compatible
;      OPERATING SYSTEM:  MS-DOS 4.01
;      SOFTWARE:  Word for Windows-t
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/898,905
;      FILING DATE:  19920612
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  none
;      FILING DATE:  none
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sundsmo,John,S.
;      REGISTRATION NUMBER:  34,446
;      REFERENCE/DOCKET NUMBER:  UOFW-1-6521
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  1-206-682-8100; 1-206-224-0727 (direct)
;      TELEFAX:  1-206-224-0779
;      TELEX:  4938023
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  851 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic DNA
;      DESCRIPTION:  Cps
US-07-898-905-3

  Query Match           100.0%;  Score 20;  DB 1;  Length 851;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db        610 GCAAACAGGATTAGATACCC 629


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Job time : 37.1446 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 06:01:54 ; Search time 39.759 Seconds
(without alignments)
307.073 Million cell updates/sec

Title: US-09-940-860-3
Perfect score: 22
Sequence: 1 acaaggcccgagaacgtattca 22

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	22	100.0	368	2	US-07-923-871C-36	Sequence 36, Appl
c 2	22	100.0	370	2	US-07-923-871C-35	Sequence 35, Appl
c 3	22	100.0	498	2	US-07-923-871C-1	Sequence 1, Appli
c 4	22	100.0	505	5	PCT-US91-01574-1	Sequence 1, Appli
c 5	22	100.0	1284	3	US-09-052-333A-26	Sequence 26, Appl
c 6	22	100.0	1284	3	US-09-052-333A-27	Sequence 27, Appl
c 7	22	100.0	1284	3	US-09-052-333A-28	Sequence 28, Appl
c 8	22	100.0	1284	3	US-09-052-333A-29	Sequence 29, Appl
c 9	22	100.0	1284	3	US-09-052-333A-31	Sequence 31, Appl
c 10	22	100.0	1408	2	US-08-632-470-40	Sequence 40, Appl
c 11	22	100.0	1427	2	US-08-632-470-27	Sequence 27, Appl
c 12	22	100.0	1432	2	US-08-632-470-25	Sequence 25, Appl
c 13	22	100.0	1432	2	US-08-632-470-32	Sequence 32, Appl
c 14	22	100.0	1436	2	US-08-632-470-34	Sequence 34, Appl
c 15	22	100.0	1438	2	US-08-632-470-24	Sequence 24, Appl
c 16	22	100.0	1439	2	US-08-632-470-31	Sequence 31, Appl
c 17	22	100.0	1439	2	US-08-632-470-42	Sequence 42, Appl
c 18	22	100.0	1440	2	US-08-632-470-23	Sequence 23, Appl
c 19	22	100.0	1440	2	US-08-632-470-26	Sequence 26, Appl
c 20	22	100.0	1440	2	US-08-632-470-28	Sequence 28, Appl
c 21	22	100.0	1440	2	US-08-632-470-29	Sequence 29, Appl
c 22	22	100.0	1440	2	US-08-632-470-33	Sequence 33, Appl
c 23	22	100.0	1440	2	US-08-632-470-35	Sequence 35, Appl
c 24	22	100.0	1440	2	US-08-632-470-36	Sequence 36, Appl
c 25	22	100.0	1440	2	US-08-632-470-37	Sequence 37, Appl
c 26	22	100.0	1440	2	US-08-632-470-39	Sequence 39, Appl
c 27	22	100.0	1440	2	US-08-632-470-41	Sequence 41, Appl
c 28	22	100.0	1440	2	US-08-632-470-43	Sequence 43, Appl
c 29	22	100.0	1440	2	US-08-632-470-46	Sequence 46, Appl
c 30	22	100.0	1441	2	US-08-632-470-38	Sequence 38, Appl
c 31	22	100.0	1442	2	US-08-632-470-30	Sequence 30, Appl
c 32	22	100.0	1458	2	US-08-632-470-45	Sequence 45, Appl
c 33	22	100.0	1484	2	US-08-632-470-53	Sequence 53, Appl
c 34	22	100.0	1508	2	US-08-632-470-44	Sequence 44, Appl
c 35	22	100.0	1230025	4	US-09-198-452A-1	Sequence 1, Appli
c 36	16	72.7	683	1	US-08-147-891-1	Sequence 1, Appli
c 37	16	72.7	683	1	US-08-943-464-1	Sequence 1, Appli
c 38	16	72.7	683	1	US-08-943-464-2	Sequence 2, Appli
c 39	16	72.7	683	4	US-09-491-384-1	Sequence 1, Appli
c 40	16	72.7	683	4	US-09-491-384-2	Sequence 2, Appli
c 41	16	72.7	683	4	US-09-061-770-1	Sequence 1, Appli
c 42	16	72.7	683	4	US-09-061-770-2	Sequence 2, Appli
c 43	16	72.7	938	2	US-08-879-128-1	Sequence 1, Appli
c 44	16	72.7	1435	2	US-08-632-470-48	Sequence 48, Appl
c 45	16	72.7	1494	2	US-08-632-470-49	Sequence 49, Appl

ALIGNMENTS

```
RESULT 1
US-07-923-871C-36/c
; Sequence 36, Application US/07923871C
; Patent No. 5912117
;  GENERAL INFORMATION:
;    APPLICANT:  White Ph.D, Thomas J.
;    APPLICANT:  Dodge, Deborah E.
;    TITLE OF INVENTION:  Method for Diagnosis of Lyme Disease
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/923,871C
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 489,676
;      FILING DATE:  07-MAR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petry, Douglas A.
;      REGISTRATION NUMBER:  35,321
;      REFERENCE/DOCKET NUMBER:  8697
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814-2974
;      TELEFAX:  (510) 814-2977
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  368 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-923-871C-36

  Query Match           100.0%;  Score 22;  DB 2;  Length 368;
  Best Local Similarity  100.0%;  Pred. No. 4e-05;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
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                    ||||||||||||||||||||
Db        273 ACAAGGCCCGAGAACGTATTCA 252


RESULT 2
US-07-923-871C-35/c
; Sequence 35, Application US/07923871C
; Patent No. 5912117
;  GENERAL INFORMATION:
;    APPLICANT:  White Ph.D, Thomas J.
;    APPLICANT:  Dodge, Deborah E.
;    TITLE OF INVENTION:  Method for Diagnosis of Lyme Disease
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/923,871C
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 489,676
;      FILING DATE:  07-MAR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petry, Douglas A.
;      REGISTRATION NUMBER:  35,321
;      REFERENCE/DOCKET NUMBER:  8697
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814-2974
;      TELEFAX:  (510) 814-2977
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  370 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-923-871C-35

  Query Match           100.0%;  Score 22;  DB 2;  Length 370;
  Best Local Similarity  100.0%;  Pred. No. 4e-05;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        275 ACAAGGCCCGAGAACGTATTCA 254


RESULT 3
US-07-923-871C-1/c
; Sequence 1, Application US/07923871C
; Patent No. 5912117
;  GENERAL INFORMATION:
;    APPLICANT:  White Ph.D, Thomas J.
;    APPLICANT:  Dodge, Deborah E.
;    TITLE OF INVENTION:  Method for Diagnosis of Lyme Disease
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/923,871C
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 489,676
;      FILING DATE:  07-MAR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petry, Douglas A.
;      REGISTRATION NUMBER:  35,321
;      REFERENCE/DOCKET NUMBER:  8697
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814-2974
;      TELEFAX:  (510) 814-2977
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  498 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (35..36)
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (41)
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (67)
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (164..165)
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (167)
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (169)
US-07-923-871C-1

  Query Match           100.0%;  Score 22;  DB 2;  Length 498;
  Best Local Similarity  100.0%;  Pred. No. 4e-05;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        396 ACAAGGCCCGAGAACGTATTCA 375


RESULT 4
PCT-US91-01574-1/c
; Sequence 1, Application PC/TUS9101574
;  GENERAL INFORMATION:
;    APPLICANT:  White Ph.D, Thomas J.
;    APPLICANT:  Dodge, Deborah E.
;    TITLE OF INVENTION:  Method for Diagnosis of Lyme Disease
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cetus Corporation
;      STREET:  1400 Fifty-Third Street
;      CITY:  Emeryville
;      STATE:  CA
;      COUNTRY:  USA
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;       ZIP:  94608
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US91/01574
;       FILING DATE:  19910307
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 489,676
;       FILING DATE:  07-MAR-1990
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Kaster, Kevin R.
;       REGISTRATION NUMBER:  32,704
;       REFERENCE/DOCKET NUMBER:  2536.1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 420-3444
;       TELEFAX:  (415) 658-5239
;       TELEX:  4992659
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  505 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FEATURE:
;       NAME/KEY:  unsure
;       LOCATION:  complement (35..36)
;     FEATURE:
;       NAME/KEY:  unsure
;       LOCATION:  complement (41)
;     FEATURE:
;       NAME/KEY:  unsure
;       LOCATION:  complement (67)
;     FEATURE:
;       NAME/KEY:  unsure
;       LOCATION:  complement (164..165)
;     FEATURE:
;       NAME/KEY:  unsure
;       LOCATION:  complement (167)
;     FEATURE:
;       NAME/KEY:  unsure
;       LOCATION:  complement (169)
PCT-US91-01574-1

  Query Match             100.0%;  Score 22;  DB 5;  Length 505;
  Best Local Similarity   100.0%;  Pred. No. 4e-05;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        396 ACAAGGCCCGAGAACGTATTCA 375


RESULT 5
US-09-052-333A-26/c
; Sequence 26, Application US/09052333A
; Patent No. 6261769
;  GENERAL INFORMATION:
;     APPLICANT:  Everett, Karin D.E.
;     APPLICANT:  Andersen, Arthur A.
;     TITLE OF INVENTION:  Intergenic Spacer Target Sequence for
; Patent No. 6261769
;     TITLE OF INVENTION:  Detecting and Distinguishing Chlamydial Strains
;     NUMBER OF SEQUENCES:  73
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Curtis P. Ribando
;       STREET:  1815 N. University Street
;       CITY:  Peoria
;       STATE:  IL
;       COUNTRY:  US
;       ZIP:  61604
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/052,333A
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Ribando, Curtis P.
;       REGISTRATION NUMBER:  27,976
;       REFERENCE/DOCKET NUMBER:  0211.97
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  309/681-6513
;       TELEFAX:  309/681-6688
;   INFORMATION FOR SEQ ID NO:  26:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1284 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  rRNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     ORIGINAL SOURCE:
;       ORGANISM:  Chlamydia pneumoniae
;       STRAIN:  CWL-029
;     FEATURE:
;       NAME/KEY:  rRNA
;       LOCATION:  1..221
;       OTHER INFORMATION:  /note= "16S rRNA"
;     FEATURE:
;       NAME/KEY:  misc_RNA
;       LOCATION:  222..444
;       OTHER INFORMATION:  /note= "intergenic spacer"
;     FEATURE:
;       NAME/KEY:  rRNA
;       LOCATION:  445..1063
;       OTHER INFORMATION:  /note= "Domain I of the 23S rRNA"
;     FEATURE:
;       NAME/KEY:  rRNA
;       LOCATION:  445..1284
;       OTHER INFORMATION:  /note= "23S rRNA"
;     FEATURE:
;       NAME/KEY:  misc_RNA
;       LOCATION:  1..537
;       OTHER INFORMATION:  /note= "Region A - Region of the
;       OTHER INFORMATION:  Intergenic Spacer"
;     FEATURE:
;       NAME/KEY:  rRNA
;       LOCATION:  959..1086
;       OTHER INFORMATION:  /note= "Region B - The 3' End of
;       OTHER INFORMATION:  Domain I in the 23S rRNA"
US-09-052-333A-26

  Query Match             100.0%;  Score 22;  DB 3;  Length 1284;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-05;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db         67 ACAAGGCCCGAGAACGTATTCA 46


RESULT 6
US-09-052-333A-27/c
; Sequence 27, Application US/09052333A
; Patent No. 6261769
```

```
;  GENERAL INFORMATION:
;    APPLICANT:  Everett, Karin D.E.
;    APPLICANT:  Andersen, Arthur A.
;    TITLE OF INVENTION:  Intergenic Spacer Target Sequence for
; Patent No. 6261769
;    TITLE OF INVENTION:  Detecting and Distinguishing Chlamydial Strains
;    NUMBER OF SEQUENCES:  73
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis P. Ribando
;      STREET:  1815 N. University Street
;      CITY:  Peoria
;      STATE:  IL
;      COUNTRY:  US
;      ZIP:  61604
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/052,333A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ribando, Curtis P.
;      REGISTRATION NUMBER:  27,976
;      REFERENCE/DOCKET NUMBER:  0211.97
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  309/681-6513
;      TELEFAX:  309/681-6688
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1284 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  rRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Chlamydia pneumoniae
;      STRAIN:  CWL-1011
;    FEATURE:
;      NAME/KEY:  rRNA
;      LOCATION:  1..221
;      OTHER INFORMATION:  /note= "16S rRNA"
;    FEATURE:
;      NAME/KEY:  misc_RNA
;      LOCATION:  222..444
;      OTHER INFORMATION:  /note= "intergenic spacer"
;    FEATURE:
;      NAME/KEY:  rRNA
;      LOCATION:  445..1063
;      OTHER INFORMATION:  /note= "Domain I of the 23S rRNA"
;    FEATURE:
;      NAME/KEY:  rRNA
;      LOCATION:  445..1284
;      OTHER INFORMATION:  /note= "23S rRNA"
;    FEATURE:
;      NAME/KEY:  misc_RNA
;      LOCATION:  1..537
;      OTHER INFORMATION:  /note= "Region A - Region of the
;      OTHER INFORMATION:  Intergenic Spacer"
;    FEATURE:
;      NAME/KEY:  rRNA
;      LOCATION:  959..1086
;      OTHER INFORMATION:  /note= "Region B - The 3' End of
;      OTHER INFORMATION:  Domain I in the 23S rRNA"
US-09-052-333A-27

  Query Match             100.0%;  Score 22;  DB 3;  Length 1284;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-05;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db         67 ACAAGGCCCGAGAACGTATTCA 46


RESULT 7
US-09-052-333A-28/c
; Sequence 28, Application US/09052333A
; Patent No. 6261769
;  GENERAL INFORMATION:
;    APPLICANT:  Everett, Karin D.E.
;    APPLICANT:  Andersen, Arthur A.
;    TITLE OF INVENTION:  Intergenic Spacer Target Sequence for
; Patent No. 6261769
;    TITLE OF INVENTION:  Detecting and Distinguishing Chlamydial Strains
;    NUMBER OF SEQUENCES:  73
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis P. Ribando
;      STREET:  1815 N. University Street
;      CITY:  Peoria
;      STATE:  IL
;      COUNTRY:  US
;      ZIP:  61604
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/052,333A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ribando, Curtis P.
;      REGISTRATION NUMBER:  27,976
;      REFERENCE/DOCKET NUMBER:  0211.97
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  309/681-6513
;      TELEFAX:  309/681-6688
;  INFORMATION FOR SEQ ID NO:  28:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1284 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  rRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Chlamydia pneumoniae
;      STRAIN:  FML-12
;    FEATURE:
;      NAME/KEY:  rRNA
;      LOCATION:  1..221
;      OTHER INFORMATION:  /note= "16S rRNA"
;    FEATURE:
;      NAME/KEY:  misc_RNA
;      LOCATION:  222..444
;      OTHER INFORMATION:  /note= "intergenic spacer"
;    FEATURE:
;      NAME/KEY:  rRNA
;      LOCATION:  445..1063
;      OTHER INFORMATION:  /note= "Domain I of the 23S rRNA"
;    FEATURE:
;      NAME/KEY:  rRNA
;      LOCATION:  445..1284
;      OTHER INFORMATION:  /note= "23S rRNA"
;    FEATURE:
;      NAME/KEY:  misc_RNA
;      LOCATION:  1..537
;      OTHER INFORMATION:  /note= "Region A - Region of the
;      OTHER INFORMATION:  Intergenic Spacer"
```

```
;    FEATURE:
;      NAME/KEY:  rRNA
;      LOCATION:  959..1086
;      OTHER INFORMATION:  /note= "Region B - The 3' End of
;      OTHER INFORMATION:  Domain I in the 23S rRNA"
US-09-052-333A-28

  Query Match             100.0%;  Score 22;  DB 3;  Length 1284;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-05;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db         67 ACAAGGCCCGAGAACGTATTCA 46


RESULT 8
US-09-052-333A-29/c
; Sequence 29, Application US/09052333A
; Patent No. 6261769
;  GENERAL INFORMATION:
;    APPLICANT:  Everett, Karin D.E.
;    APPLICANT:  Andersen, Arthur A.
;    TITLE OF INVENTION:  Intergenic Spacer Target Sequence for
; Patent No. 6261769
;    TITLE OF INVENTION:  Detecting and Distinguishing Chlamydial Strains
;    NUMBER OF SEQUENCES:  73
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis P. Ribando
;      STREET:  1815 N. University Street
;      CITY:  Peoria
;      STATE:  IL
;      COUNTRY:  US
;      ZIP:  61604
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/052,333A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ribando, Curtis P.
;      REGISTRATION NUMBER:  27,976
;      REFERENCE/DOCKET NUMBER:  0211.97
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  309/681-6513
;      TELEFAX:  309/681-6688
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1284 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  rRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Chlamydia pneumoniae
;      STRAIN:  FML-16
;    FEATURE:
;      NAME/KEY:  rRNA
;      LOCATION:  1..221
;      OTHER INFORMATION:  /note= "16S rRNA"
;    FEATURE:
;      NAME/KEY:  misc_RNA
;      LOCATION:  222..444
;      OTHER INFORMATION:  /note= "intergenic spacer"
;    FEATURE:
;      NAME/KEY:  rRNA
;      LOCATION:  445..1063
;      OTHER INFORMATION:  /note= "Domain I of the 23S rRNA"
;    FEATURE:
;      NAME/KEY:  rRNA
;      LOCATION:  445..1284
;      OTHER INFORMATION:  /note= "23S rRNA"
;    FEATURE:
;      NAME/KEY:  misc_RNA
;      LOCATION:  1..537
;      OTHER INFORMATION:  /note= "Region A - Region of the
;      OTHER INFORMATION:  Intergenic Spacer"
;    FEATURE:
;      NAME/KEY:  rRNA
;      LOCATION:  959..1086
;      OTHER INFORMATION:  /note= "Region B - The 3' End of
;      OTHER INFORMATION:  Domain I in the 23S rRNA"
US-09-052-333A-29

  Query Match             100.0%;  Score 22;  DB 3;  Length 1284;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-05;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db         67 ACAAGGCCCGAGAACGTATTCA 46


RESULT 9
US-09-052-333A-31/c
; Sequence 31, Application US/09052333A
; Patent No. 6261769
;  GENERAL INFORMATION:
;    APPLICANT:  Everett, Karin D.E.
;    APPLICANT:  Andersen, Arthur A.
;    TITLE OF INVENTION:  Intergenic Spacer Target Sequence for
; Patent No. 6261769
;    TITLE OF INVENTION:  Detecting and Distinguishing Chlamydial Strains
;    NUMBER OF SEQUENCES:  73
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis P. Ribando
;      STREET:  1815 N. University Street
;      CITY:  Peoria
;      STATE:  IL
;      COUNTRY:  US
;      ZIP:  61604
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/052,333A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ribando, Curtis P.
;      REGISTRATION NUMBER:  27,976
;      REFERENCE/DOCKET NUMBER:  0211.97
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  309/681-6513
;      TELEFAX:  309/681-6688
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1284 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  rRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Chlamydia pneumoniae
;      STRAIN:  TW-183
;    FEATURE:
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;      NAME/KEY:  rRNA
;      LOCATION:  1..221
;      OTHER INFORMATION:  /note= "16S rRNA"
;    FEATURE:
;      NAME/KEY:  misc_RNA
;      LOCATION:  222..444
;      OTHER INFORMATION:  /note= "intergenic spacer"
;    FEATURE:
;      NAME/KEY:  rRNA
;      LOCATION:  445..1063
;      OTHER INFORMATION:  /note= "Domain I of the 23S rRNA"
;    FEATURE:
;      NAME/KEY:  rRNA
;      LOCATION:  445..1284
;      OTHER INFORMATION:  /note= "23S rRNA"
;    FEATURE:
;      NAME/KEY:  misc_RNA
;      LOCATION:  1..537
;      OTHER INFORMATION:  /note= "Region A - Region of the
;      OTHER INFORMATION:  Intergenic Spacer"
;    FEATURE:
;      NAME/KEY:  rRNA
;      LOCATION:  959..1086
;      OTHER INFORMATION:  /note= "Region B - The 3' End of
;      OTHER INFORMATION:  Domain I in the 23S rRNA"
US-09-052-333A-31

  Query Match           100.0%;  Score 22;  DB 3;  Length 1284;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-05;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
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Db         67 ACAAGGCCCGAGAACGTATTCA 46


RESULT 10
US-08-632-470-40/c
; Sequence 40, Application US/08632470
; Patent No. 5976791
;  GENERAL INFORMATION:
;    APPLICANT:  MABILAT, CLAUDE
;    APPLICANT:  RAOULT, DIDIER
;    TITLE OF INVENTION:  NUCLEOTIDE FRAGMENTS CAPABLE OF
;    TITLE OF INVENTION:  HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
;    TITLE OF INVENTION:  THEIR USE AS PROBES OR PRIMERS
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OLIFF & BERRIDGE
;      STREET:  P.O. BOX 19928
;      CITY:  ALEXANDRIA
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22320
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/632,470
;      FILING DATE:  08-JUL-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BERRIDGE, WILLIAM P
;      REGISTRATION NUMBER:  30,024
;      REFERENCE/DOCKET NUMBER:  WPB 38238
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)-836-6400
;      TELEFAX:  (703)-836-2787
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1408 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-632-470-40

  Query Match           100.0%;  Score 22;  DB 2;  Length 1408;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-05;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db       1319 ACAAGGCCCGAGAACGTATTCA 1298


RESULT 11
US-08-632-470-27/c
; Sequence 27, Application US/08632470
; Patent No. 5976791
;  GENERAL INFORMATION:
;    APPLICANT:  MABILAT, CLAUDE
;    APPLICANT:  RAOULT, DIDIER
;    TITLE OF INVENTION:  NUCLEOTIDE FRAGMENTS CAPABLE OF
;    TITLE OF INVENTION:  HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
;    TITLE OF INVENTION:  THEIR USE AS PROBES OR PRIMERS
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OLIFF & BERRIDGE
;      STREET:  P.O. BOX 19928
;      CITY:  ALEXANDRIA
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22320
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/632,470
;      FILING DATE:  08-JUL-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BERRIDGE, WILLIAM P
;      REGISTRATION NUMBER:  30,024
;      REFERENCE/DOCKET NUMBER:  WPB 38238
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)-836-6400
;      TELEFAX:  (703)-836-2787
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1427 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-632-470-27

  Query Match           100.0%;  Score 22;  DB 2;  Length 1427;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-05;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db       1322 ACAAGGCCCGAGAACGTATTCA 1301


RESULT 12
US-08-632-470-25/c
; Sequence 25, Application US/08632470
; Patent No. 5976791
;  GENERAL INFORMATION:
;    APPLICANT:  MABILAT, CLAUDE
```

```
;    APPLICANT:  RAOULT, DIDIER
;    TITLE OF INVENTION:  NUCLEOTIDE FRAGMENTS CAPABLE OF
;    TITLE OF INVENTION:  HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
;    TITLE OF INVENTION:  THEIR USE AS PROBES OR PRIMERS
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OLIFF & BERRIDGE
;      STREET:  P.O. BOX 19928
;      CITY:  ALEXANDRIA
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22320
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/632,470
;      FILING DATE:  08-JUL-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BERRIDGE, WILLIAM P
;      REGISTRATION NUMBER:  30,024
;      REFERENCE/DOCKET NUMBER:  WPB 38238
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)-836-6400
;      TELEFAX:  (703)-836-2787
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-632-470-25

  Query Match            100.0%;  Score 22;  DB 2;  Length 1432;
  Best Local Similarity  100.0%;  Pred. No. 3.9e-05;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db       1327 ACAAGGCCCGAGAACGTATTCA 1306


RESULT 13
US-08-632-470-32/c
; Sequence 32, Application US/08632470
; Patent No. 5976791
;  GENERAL INFORMATION:
;    APPLICANT:  MABILAT, CLAUDE
;    APPLICANT:  RAOULT, DIDIER
;    TITLE OF INVENTION:  NUCLEOTIDE FRAGMENTS CAPABLE OF
;    TITLE OF INVENTION:  HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
;    TITLE OF INVENTION:  THEIR USE AS PROBES OR PRIMERS
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OLIFF & BERRIDGE
;      STREET:  P.O. BOX 19928
;      CITY:  ALEXANDRIA
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22320
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/632,470
;      FILING DATE:  08-JUL-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BERRIDGE, WILLIAM P
;      REGISTRATION NUMBER:  30,024
;      REFERENCE/DOCKET NUMBER:  WPB 38238
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)-836-6400
;      TELEFAX:  (703)-836-2787
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-632-470-32

  Query Match            100.0%;  Score 22;  DB 2;  Length 1432;
  Best Local Similarity  100.0%;  Pred. No. 3.9e-05;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db       1327 ACAAGGCCCGAGAACGTATTCA 1306


RESULT 14
US-08-632-470-34/c
; Sequence 34, Application US/08632470
; Patent No. 5976791
;  GENERAL INFORMATION:
;    APPLICANT:  MABILAT, CLAUDE
;    APPLICANT:  RAOULT, DIDIER
;    TITLE OF INVENTION:  NUCLEOTIDE FRAGMENTS CAPABLE OF
;    TITLE OF INVENTION:  HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
;    TITLE OF INVENTION:  THEIR USE AS PROBES OR PRIMERS
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OLIFF & BERRIDGE
;      STREET:  P.O. BOX 19928
;      CITY:  ALEXANDRIA
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22320
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/632,470
;      FILING DATE:  08-JUL-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BERRIDGE, WILLIAM P
;      REGISTRATION NUMBER:  30,024
;      REFERENCE/DOCKET NUMBER:  WPB 38238
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)-836-6400
;      TELEFAX:  (703)-836-2787
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1436 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-632-470-34

  Query Match            100.0%;  Score 22;  DB 2;  Length 1436;
  Best Local Similarity  100.0%;  Pred. No. 3.9e-05;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
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```
                    ||||||||||||||||||||
Db       1331 ACAAGGCCCGAGAACGTATTCA 1310


RESULT 15
US-08-632-470-24/c
; Sequence 24, Application US/08632470
; Patent No. 5976791
;  GENERAL INFORMATION:
;    APPLICANT:  MABILAT, CLAUDE
;    APPLICANT:  RAOULT, DIDIER
;    TITLE OF INVENTION:  NUCLEOTIDE FRAGMENTS CAPABLE OF
;    TITLE OF INVENTION:  HYBRIDIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
;    TITLE OF INVENTION:  THEIR USE AS PROBES OR PRIMERS
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OLIFF & BERRIDGE
;      STREET:  P.O. BOX 19928
;      CITY:  ALEXANDRIA
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22320
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/632,470
;      FILING DATE:  08-JUL-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BERRIDGE, WILLIAM P
;      REGISTRATION NUMBER:  30,024
;      REFERENCE/DOCKET NUMBER:  WPB 38238
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)-836-6400
;      TELEFAX:  (703)-836-2787
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1438 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-632-470-24

  Query Match             100.0%;  Score 22;  DB 2;  Length 1438;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-05;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
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Db       1333 ACAAGGCCCGAGAACGTATTCA 1312


Search completed: August  4, 2004, 09:23:29
Job time : 40.759 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 06:01:54 ; Search time 36.1446 Seconds
(without alignments)
307.073 Million cell updates/sec

Title: US-09-940-860-2
Perfect score: 20
Sequence: 1 ggaggaaggcgaggatgacg 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	1548	4	US-09-726-774-11	Sequence 11, Appl
	2	20	100.0	2751	3	US-09-052-333A-6	Sequence 6, Appli
	3	20	100.0	2762	3	US-09-052-333A-37	Sequence 37, Appl
	4	20	100.0	1230025	4	US-09-198-452A-1	Sequence 1, Appli
	5	16	80.0	420	4	US-09-252-991A-11029	Sequence 11029, A
c	6	16	80.0	1107	4	US-09-252-991A-13336	Sequence 13336, A
c	7	16	80.0	1179	4	US-09-252-991A-13193	Sequence 13193, A
	8	16	80.0	1308	4	US-09-252-991A-12614	Sequence 12614, A
c	9	16	80.0	1683	4	US-09-252-991A-11226	Sequence 11226, A
c	10	16	80.0	1974	4	US-09-252-991A-11111	Sequence 11111, A
	11	16	80.0	2283	4	US-09-252-991A-10956	Sequence 10956, A
c	12	15	75.0	191	4	US-09-621-976-8573	Sequence 8573, Ap
	13	15	75.0	752	3	US-08-818-112-2	Sequence 2, Appli
	14	15	75.0	752	4	US-08-818-111-2	Sequence 2, Appli
	15	15	75.0	752	4	US-09-056-556-2	Sequence 2, Appli
	16	15	75.0	752	4	US-09-072-596-2	Sequence 2, Appli
	17	15	75.0	752	4	US-09-072-967-2	Sequence 2, Appli
	18	15	75.0	889	4	US-09-050-739-5	Sequence 5, Appli
c	19	15	75.0	1245	4	US-09-252-991A-6286	Sequence 6286, Ap
c	20	15	75.0	1980	4	US-09-252-991A-6369	Sequence 6369, Ap
	21	15	75.0	2499	4	US-09-252-991A-6182	Sequence 6182, Ap
	22	15	75.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	23	15	75.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	24	14	70.0	396	4	US-09-252-991A-6707	Sequence 6707, Ap
c	25	14	70.0	541	4	US-09-743-207-13	Sequence 13, Appl
	26	14	70.0	738	4	US-09-252-991A-2237	Sequence 2237, Ap
c	27	14	70.0	885	4	US-09-252-991A-10382	Sequence 10382, A
c	28	14	70.0	1206	4	US-09-489-039A-4798	Sequence 4798, Ap
c	29	14	70.0	1260	4	US-09-252-991A-6674	Sequence 6674, Ap
	30	14	70.0	1717	4	US-09-673-395A-11	Sequence 11, Appl
c	31	14	70.0	1734	4	US-09-252-991A-2607	Sequence 2607, Ap
c	32	14	70.0	2016	4	US-09-252-991A-2445	Sequence 2445, Ap
	33	14	70.0	2141	4	US-09-620-312D-635	Sequence 635, App
c	34	14	70.0	2163	4	US-09-252-991A-6641	Sequence 6641, Ap
c	35	14	70.0	2169	4	US-09-252-991A-10268	Sequence 10268, A
	36	14	70.0	2637	4	US-09-735-934A-1	Sequence 1, Appli
	37	14	70.0	2637	4	US-10-060-332-1	Sequence 1, Appli
c	38	14	70.0	3437	3	US-08-450-962-3	Sequence 3, Appli
c	39	14	70.0	3437	4	US-08-848-631-3	Sequence 3, Appli
	40	14	70.0	8906	2	US-08-826-267-1	Sequence 1, Appli
c	41	14	70.0	17138	3	US-09-813-819-3	Sequence 3, Appli
c	42	14	70.0	17138	4	US-09-920-048-3	Sequence 3, Appli
	43	14	70.0	43950	4	US-09-735-934A-3	Sequence 3, Appli
	44	14	70.0	43950	4	US-10-060-332-3	Sequence 3, Appli
c	45	13	65.0	20	4	US-09-302-681-91	Sequence 91, Appl

ALIGNMENTS

RESULT 1
US-09-726-774-11
; Sequence 11, Application US/09726774
; Patent No. 6677153
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; TITLE OF INVENTION: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/09/726,774
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-09-726-774-11

Query Match 100.0%; Score 20; DB 4; Length 1548;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GGAGGAAGGCGAGGATGACG 20
              ||||||||||||||||||||
Db       1179 GGAGGAAGGCGAGGATGACG 1198
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RESULT 2
US-09-052-333A-6
; Sequence 6, Application US/09052333A
; Patent No. 6261769
; GENERAL INFORMATION:
; APPLICANT: Everett, Karin D.E.
; APPLICANT: Andersen, Arthur A.
; TITLE OF INVENTION: Intergenic Spacer Target Sequence for
; Patent No. 6261769
; TITLE OF INVENTION: Detecting and Distinguishing Chlamydial Strains
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis P. Ribando
; STREET: 1815 N. University Street
; CITY: Peoria
; STATE: IL
; COUNTRY: US
; ZIP: 61604
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/052,333A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ribando, Curtis P.
;      REGISTRATION NUMBER:  27,976
;      REFERENCE/DOCKET NUMBER:  0211.97
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  309/681-6513
;      TELEFAX:  309/681-6688
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2751 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  rRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Chlamydia psittaci
;      STRAIN:  NJ1
;    FEATURE:
;      NAME/KEY:  rRNA
;      LOCATION:  1..564
;      OTHER INFORMATION:  /note= "16S rRNA"
;    FEATURE:
;      NAME/KEY:  misc_RNA
;      LOCATION:  565..788
;      OTHER INFORMATION:  /note= "intergenic spacer"
;    FEATURE:
;      NAME/KEY:  rRNA
;      LOCATION:  789..1409
;      OTHER INFORMATION:  /note= "Domain I of the 23S rRNA"
;    FEATURE:
;      NAME/KEY:  rRNA
;      LOCATION:  789..2751
;      OTHER INFORMATION:  /note= "23S rRNA"
;    FEATURE:
;      NAME/KEY:  misc_RNA
;      LOCATION:  346..881
;      OTHER INFORMATION:  /note= "Region A - Region of the
;      OTHER INFORMATION:  Intergenic Spacer"
;    FEATURE:
;      NAME/KEY:  rRNA
;      LOCATION:  1303..1432
;      OTHER INFORMATION:  /note= "Region B - The 3' End of
;      OTHER INFORMATION:  Domain I in the 23S rRNA"
US-09-052-333A-6

  Query Match             100.0%;  Score 20;  DB 3;  Length 2751;
  Best Local Similarity   100.0%;  Pred. No. 0.015;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
              ||||||||||||||||||||
Db        193 GGAGGAAGGCGAGGATGACG 212


RESULT 3
US-09-052-333A-37
; Sequence 37, Application US/09052333A
; Patent No. 6261769
;  GENERAL INFORMATION:
;    APPLICANT:  Everett, Karin D.E.
;    APPLICANT:  Andersen, Arthur A.
;    TITLE OF INVENTION:  Intergenic Spacer Target Sequence for
; Patent No. 6261769
;    TITLE OF INVENTION:  Detecting and Distinguishing Chlamydial Strains
;    NUMBER OF SEQUENCES:  73
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis P. Ribando
;      STREET:  1815 N. University Street
;      CITY:  Peoria
;      STATE:  IL
;      COUNTRY:  US
;      ZIP:  61604
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/052,333A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ribando, Curtis P.
;      REGISTRATION NUMBER:  27,976
;      REFERENCE/DOCKET NUMBER:  0211.97
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  309/681-6513
;      TELEFAX:  309/681-6688
;  INFORMATION FOR SEQ ID NO:  37:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2762 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  rRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Chlamydia trachomatis
;      STRAIN:  R22
;    FEATURE:
;      NAME/KEY:  rRNA
;      LOCATION:  1..564
;      OTHER INFORMATION:  /note= "16S rRNA"
;    FEATURE:
;      NAME/KEY:  misc_RNA
;      LOCATION:  565..802
;      OTHER INFORMATION:  /note= "intergenic spacer"
;    FEATURE:
;      NAME/KEY:  rRNA
;      LOCATION:  803..1424
;      OTHER INFORMATION:  /note= "Domain I of the 23S rRNA"
;    FEATURE:
;      NAME/KEY:  rRNA
;      LOCATION:  803..2762
;      OTHER INFORMATION:  /note= "23S rRNA"
;    FEATURE:
;      NAME/KEY:  misc_RNA
;      LOCATION:  346..895
;      OTHER INFORMATION:  /note= "Region A - Region of the
;      OTHER INFORMATION:  Intergenic Spacer"
;    FEATURE:
;      NAME/KEY:  rRNA
;      LOCATION:  1320..1447
;      OTHER INFORMATION:  /note= "Region B - The 3' End of
;      OTHER INFORMATION:  Domain I in the 23S rRNA"
US-09-052-333A-37

  Query Match             100.0%;  Score 20;  DB 3;  Length 2762;
  Best Local Similarity   100.0%;  Pred. No. 0.015;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
              ||||||||||||||||||||
Db        193 GGAGGAAGGCGAGGATGACG 212
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```
RESULT 4
US-09-198-452A-1
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/09/198,452A
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
;   LENGTH: 1230025
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (15001)..(30000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (30001)..(45000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (45001)..(60000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (60001)..(75000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (75001)..(90000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (90001)..(105000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (105001)..(120000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (120001)..(135000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (135001)..(150000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (150001)..(165000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (165001)..(180000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (180001)..(195000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (195001)..(210000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (210001)..(225000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (225001)..(240000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (240001)..(255000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (255001)..(270000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (270001)..(285000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (285001)..(300000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (300001)..(315000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (315001)..(330000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (330001)..(345000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (345001)..(360000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (360001)..(375000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (375001)..(390000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (390001)..(405000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (405001)..(420000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (420001)..(435000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (435001)..(450000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (450001)..(465000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (465001)..(480000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (480001)..(495000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (495001)..(510000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (510001)..(525000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (525001)..(540000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (540001)..(555000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (555001)..(570000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (570001)..(585000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (585001)..(600000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (600001)..(615000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (615001)..(630000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (630001)..(645000)
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;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (645001)..(660000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (660001)..(675000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (675001)..(690000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (690001)..(705000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (705001)..(720000)
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;   NAME/KEY: misc_feature
;   LOCATION: (720001)..(735000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (735001)..(750000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (750001)..(765000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (765001)..(780000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (780001)..(795000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (795001)..(810000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (810001)..(825000)
;   OTHER INFORMATION: n=a or c or g or t
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;   NAME/KEY: misc_feature
;   LOCATION: (855001)..(870000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (870001)..(885000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature
;   LOCATION: (885001)..(900000)
;   OTHER INFORMATION: n=a or c or g or t
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;   LOCATION: (900001)..(915000)
;   OTHER INFORMATION: n=a or c or g or t
;   NAME/KEY: misc_feature

  Query Match             100.0%;  Score 20;  DB 4;  Length 1230025;
  Best Local Similarity   100.0%;  Pred. No. 0.014;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
              ||||||||||||||||||||
Db    1011866 GGAGGAAGGCGAGGATGACG 1011885


RESULT 5
US-09-252-991A-11029
; Sequence 11029, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 11029
;   LENGTH: 420
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11029

  Query Match             80.0%;  Score 16;  DB 4;  Length 420;
  Best Local Similarity   100.0%;  Pred. No. 2.4;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 AGGAAGGCGAGGATGA 18
              ||||||||||||||||
Db        157 AGGAAGGCGAGGATGA 172


RESULT 6
US-09-252-991A-13336/c
; Sequence 13336, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 13336
;   LENGTH: 1107
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13336

  Query Match             80.0%;  Score 16;  DB 4;  Length 1107;
  Best Local Similarity   100.0%;  Pred. No. 2.4;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GAAGGCGAGGATGACG 20
              ||||||||||||||||
Db        138 GAAGGCGAGGATGACG 123


RESULT 7
US-09-252-991A-13193/c
; Sequence 13193, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 13193
;   LENGTH: 1179
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; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13193

Query Match 80.0%; Score 16; DB 4; Length 1179;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GAAGGCGAGGATGACG 20
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Db 196 GAAGGCGAGGATGACG 181

RESULT 8
US-09-252-991A-12614
; Sequence 12614, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12614
; LENGTH: 1308
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12614

Query Match 80.0%; Score 16; DB 4; Length 1308;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GAAGGCGAGGATGACG 20
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Db 1216 GAAGGCGAGGATGACG 1231

RESULT 9
US-09-252-991A-11226/c
; Sequence 11226, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 11226
; LENGTH: 1683
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11226

Query Match 80.0%; Score 16; DB 4; Length 1683;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AGGAAGGCGAGGATGA 18
||||||||||||||||
Db 1089 AGGAAGGCGAGGATGA 1074

RESULT 10
US-09-252-991A-11111/c
; Sequence 11111, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 11111
; LENGTH: 1974
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11111

Query Match 80.0%; Score 16; DB 4; Length 1974;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AGGAAGGCGAGGATGA 18
||||||||||||||||
Db 956 AGGAAGGCGAGGATGA 941

RESULT 11
US-09-252-991A-10956
; Sequence 10956, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 10956
; LENGTH: 2283
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10956

Query Match 80.0%; Score 16; DB 4; Length 2283;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AGGAAGGCGAGGATGA 18
||||||||||||||||
Db 1856 AGGAAGGCGAGGATGA 1871

RESULT 12
US-09-621-976-8573/c
; Sequence 8573, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

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;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 8573
;   LENGTH: 191
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 2
;   OTHER INFORMATION: n=a, g, c or t
US-09-621-976-8573

  Query Match          75.0%;  Score 15;  DB 4;  Length 191;
  Best Local Similarity  100.0%;  Pred. No. 8.7;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGA 15
              |||||||||||||||
Db        188 GGAGGAAGGCGAGGA 174


RESULT 13
US-08-818-112-2
; Sequence 2, Application US/08818112
; Patent No. 6290969
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, Steven G.
;    APPLICANT:  Skeiky, Yasir A.W.
;    APPLICANT:  Dillon, Davin C.
;    APPLICANT:  Campos-Neto, Antonio
;    APPLICANT:  Houghton, Raymond
;    APPLICANT:  Vedvick, Thomas S.
;    APPLICANT:  Twardzik, Daniel R.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
;    TITLE OF INVENTION:  AND DIAGNOSIS OF TUBERCULOSIS
;    NUMBER OF SEQUENCES:  153
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/818,112
;      FILING DATE:  13-MAR-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.411C6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  752 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-818-112-2

  Query Match          75.0%;  Score 15;  DB 3;  Length 752;
  Best Local Similarity  100.0%;  Pred. No. 8.5;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 AAGGCGAGGATGACG 20
              |||||||||||||||
Db        434 AAGGCGAGGATGACG 448


RESULT 14
US-08-818-111-2
; Sequence 2, Application US/08818111
; Patent No. 6338852
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, Steven G.
;    APPLICANT:  Skeiky, Yasir A.W.
;    APPLICANT:  Dillon, Davin C.
;    APPLICANT:  Campos-Neto, Antonia
;    APPLICANT:  Houghton, Raymond
;    APPLICANT:  Vedvick, Thomas S.
;    APPLICANT:  Twardzik, Daniel R.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR DIAGNOSIS OF    TUBERCULOSIS
;    NUMBER OF SEQUENCES:  148
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/818,111
;      FILING DATE:  13-MAR-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.417C6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  752 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-818-111-2

  Query Match          75.0%;  Score 15;  DB 4;  Length 752;
  Best Local Similarity  100.0%;  Pred. No. 8.5;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 AAGGCGAGGATGACG 20
              |||||||||||||||
Db        434 AAGGCGAGGATGACG 448


RESULT 15
US-09-056-556-2
; Sequence 2, Application US/09056556
; Patent No. 6350456
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, Steven G.
;    APPLICANT:  Skeiky, Yasir A.W.
;    APPLICANT:  Dillon, Davin C.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR THE PREVENTION AND          TREATM
;    NUMBER OF SEQUENCES:  241
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
```

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;       CITY:  Seattle
;       STATE:  Washington
;       COUNTRY:  USA
;       ZIP:  98104-7092
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/056,556
;       FILING DATE:  07-APR-1998
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Maki, David J.
;       REGISTRATION NUMBER:  31,392
;       REFERENCE/DOCKET NUMBER:  210121.457
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206) 622-4900
;       TELEFAX:  (206) 682-6031
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  752 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-09-056-556-2

  Query Match             75.0%;  Score 15;  DB 4;  Length 752;
  Best Local Similarity   100.0%;  Pred. No. 8.5;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 AAGGCGAGGATGACG 20
              |||||||||||||||
Db        434 AAGGCGAGGATGACG 448


Search completed: August  4, 2004, 09:23:28
Job time : 42.1446 secs
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 07:44:29 ; Search time 190.012 Seconds
(without alignments)
541.892 Million cell updates/sec

Title: US-09-940-860-4
Perfect score: 21
Sequence: 1 gtgccagcagcagcggtaata 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3222919 seqs, 2451570024 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
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18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	21	100.0	21	11	US-09-940-860-4	Sequence 4, Appli
c	2	17	81.0	1980	17	US-10-437-963-78545	Sequence 78545, A
c	3	17	81.0	3502	16	US-10-369-493-27667	Sequence 27667, A
	4	16	76.2	407	10	US-09-535-459-1484	Sequence 1484, Ap
c	5	16	76.2	600	17	US-10-021-323-3179	Sequence 3179, Ap
	6	16	76.2	1119	10	US-09-919-197-10	Sequence 10, Appl
c	7	16	76.2	1350	13	US-10-425-114-35039	Sequence 35039, A
c	8	16	76.2	1837	17	US-10-437-963-1280	Sequence 1280, Ap
c	9	16	76.2	1992	13	US-09-854-867-352	Sequence 352, App
c	10	16	76.2	2329	13	US-10-425-114-1420	Sequence 1420, Ap
	11	16	76.2	3672	13	US-10-282-122A-31366	Sequence 31366, A
c	12	15	71.4	280	10	US-09-535-459-1477	Sequence 1477, Ap
c	13	15	71.4	296	10	US-09-535-459-1478	Sequence 1478, Ap
c	14	15	71.4	364	10	US-09-535-459-1475	Sequence 1475, Ap
c	15	15	71.4	391	10	US-09-535-459-1479	Sequence 1479, Ap
	16	15	71.4	483	17	US-10-437-963-41773	Sequence 41773, A
	17	15	71.4	493	13	US-10-027-632-137746	Sequence 137746,
	18	15	71.4	493	13	US-10-027-632-137747	Sequence 137747,
	19	15	71.4	493	13	US-10-027-632-137748	Sequence 137748,
	20	15	71.4	493	16	US-10-027-632-137746	Sequence 137746,
	21	15	71.4	493	16	US-10-027-632-137747	Sequence 137747,
	22	15	71.4	493	16	US-10-027-632-137748	Sequence 137748,
c	23	15	71.4	554	10	US-09-535-459-1481	Sequence 1481, Ap
c	24	15	71.4	562	13	US-10-424-599-124900	Sequence 124900,
c	25	15	71.4	590	17	US-10-021-323-3413	Sequence 3413, Ap
	26	15	71.4	650	13	US-10-027-632-215667	Sequence 215667,
	27	15	71.4	650	13	US-10-027-632-215668	Sequence 215668,
	28	15	71.4	650	16	US-10-027-632-215667	Sequence 215667,
	29	15	71.4	650	16	US-10-027-632-215668	Sequence 215668,
	30	15	71.4	725	17	US-10-333-184-527	Sequence 527, App
c	31	15	71.4	817	17	US-10-437-963-70931	Sequence 70931, A
	32	15	71.4	845	13	US-10-027-632-164886	Sequence 164886,
	33	15	71.4	845	13	US-10-027-632-164887	Sequence 164887,
	34	15	71.4	845	13	US-10-027-632-164888	Sequence 164888,
	35	15	71.4	845	16	US-10-027-632-164886	Sequence 164886,
	36	15	71.4	845	16	US-10-027-632-164887	Sequence 164887,
	37	15	71.4	845	16	US-10-027-632-164888	Sequence 164888,
c	38	15	71.4	908	12	US-10-152-319A-2049	Sequence 2049, Ap
c	39	15	71.4	945	13	US-10-425-114-12225	Sequence 12225, A
	40	15	71.4	965	13	US-10-425-114-16650	Sequence 16650, A
c	41	15	71.4	1167	13	US-10-389-647-211	Sequence 211, App
c	42	15	71.4	1173	13	US-10-282-122A-33705	Sequence 33705, A
c	43	15	71.4	1197	16	US-10-369-493-34553	Sequence 34553, A
c	44	15	71.4	1251	13	US-10-425-114-17503	Sequence 17503, A
c	45	15	71.4	1575	16	US-10-408-167A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-940-860-4
; Sequence 4, Application US/09940860
; Publication No. US20040005555A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, Richard
; APPLICANT: Majmudar, Maulik
; TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
; FILE REFERENCE: 01107.00185
; CURRENT APPLICATION NUMBER: US/09/940,860
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/229,376
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic amplification primer
US-09-940-860-4

Query Match 100.0%; Score 21; DB 11; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GTGCCAGCAGCAGCGGTAATA 21
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Db          1 GTGCCAGCAGCAGCGGTAATA 21
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RESULT 2
US-10-437-963-78545/c
; Sequence 78545, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 78545
; LENGTH: 1980
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_78341C.1
US-10-437-963-78545

Query Match 81.0%; Score 17; DB 17; Length 1980;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGCAGCAGCGGTAATA 21
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Db 1018 CAGCAGCAGCGGTAATA 1002

RESULT 3
US-10-369-493-27667/c
; Sequence 27667, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 27667
; LENGTH: 3502
; TYPE: DNA
; ORGANISM: Neurospora crassa
US-10-369-493-27667

Query Match 81.0%; Score 17; DB 16; Length 3502;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGCCAGCAGCAGCGGTA 18
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Db 3389 TGCCAGCAGCAGCGGTA 3373

RESULT 4
US-09-535-459-1484
; Sequence 1484, Application US/09535459
; Publication No. US20030040615A1
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE
; FILE REFERENCE: PD-1014 CIP
; CURRENT APPLICATION NUMBER: US/09/535,459
; CURRENT FILING DATE: 2000-03-24
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2170
; SOFTWARE: PERL Program
; SEQ ID NO 1484
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030040615A1 hu01212406
US-09-535-459-1484

Query Match 76.2%; Score 16; DB 10; Length 407;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGCCAGCAGCAGCGGT 17
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Db 35 TGCCAGCAGCAGCGGT 50

RESULT 5
US-10-021-323-3179/c
; Sequence 3179, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 3179
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3825-023-Q6-K6-G3
US-10-021-323-3179

Query Match 76.2%; Score 16; DB 17; Length 600;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCCAGCAGCAGCGGTA 18
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Db 52 GCCAGCAGCAGCGGTA 37

RESULT 6
US-09-919-197-10
; Sequence 10, Application US/09919197
; Publication No. US20030083484A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHORT HETERODIMER PARTNER-1 EXPRESSION
; FILE REFERENCE: ISPH-0593
; CURRENT APPLICATION NUMBER: US/09/919,197
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 89

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;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 1119
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (33)...(815)
US-09-919-197-10

  Query Match             76.2%;  Score 16;  DB 10;  Length 1119;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGG 16
              ||||||||||||||||
Db        161 GTGCCAGCAGCAGCGG 176


RESULT 7
US-10-425-114-35039/c
; Sequence 35039, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 35039
;   LENGTH: 1350
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mexicana
;   FEATURE:
;   OTHER INFORMATION: Clone ID: UC-ZMFLTEOSINTE032D03_FLI
US-10-425-114-35039

  Query Match             76.2%;  Score 16;  DB 13;  Length 1350;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GCCAGCAGCAGCGGTA 18
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Db        170 GCCAGCAGCAGCGGTA 155


RESULT 8
US-10-437-963-1280/c
; Sequence 1280, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Wu, Wei
;  APPLICANT:  Boukharov, Andrey A.
;  APPLICANT:  Barbazuk, Brad
;  APPLICANT:  Li, Ping
;  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53221)B
;  CURRENT APPLICATION NUMBER: US/10/437,963
;  CURRENT FILING DATE:  2003-05-14
;  NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 1280
;   LENGTH: 1837
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(1837)
;   OTHER INFORMATION: unsure at all n locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_101161C.1
US-10-437-963-1280

  Query Match             76.2%;  Score 16;  DB 17;  Length 1837;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGG 16
              ||||||||||||||||
Db       1403 GTGCCAGCAGCAGCGG 1388


RESULT 9
US-09-854-867-352/c
; Sequence 352, Application US/09854867
; Publication No. US20030224356A1
; GENERAL INFORMATION:
;  APPLICANT: JOAN, KNOLL H
;  APPLICANT:  ROGAN, PETER K
;  TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATIN
;  FILE REFERENCE: 30307
;  CURRENT APPLICATION NUMBER: US/09/854,867
;  CURRENT FILING DATE:  2003-05-08
;  NUMBER OF SEQ ID NOS: 613
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 352
;   LENGTH: 1992
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: repeat_region
;   LOCATION: (1)..(1992)
;   OTHER INFORMATION: 11pa15_5
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (760)..(760)
;   OTHER INFORMATION: n is a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1149)..(1149)
;   OTHER INFORMATION: n is a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1261)..(1261)
;   OTHER INFORMATION: n is a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1418)..(1418)
;   OTHER INFORMATION: n is a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1533)..(1533)
;   OTHER INFORMATION: n is a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1558)..(1558)
;   OTHER INFORMATION: n is a, c, g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1802)..(1802)
;   OTHER INFORMATION: n is a, c, g or t
US-09-854-867-352

  Query Match             76.2%;  Score 16;  DB 13;  Length 1992;
  Best Local Similarity   100.0%;  Pred. No. 13;
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  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1317 GTGCCAGCAGCAGCGG 1302


RESULT 10
US-10-425-114-1420/c
; Sequence 1420, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 1420
;   LENGTH: 2329
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 700152520_FLI
US-10-425-114-1420

  Query Match             76.2%;  Score 16;  DB 13;  Length 2329;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GCCAGCAGCAGCGGTA 18
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Db       1763 GCCAGCAGCAGCGGTA 1748


RESULT 11
US-10-282-122A-31366
; Sequence 31366, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT:  Zamudio, Carlos
;  APPLICANT:  Malone, Cheryl
;  APPLICANT:  Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari
;  APPLICANT:  Zyskind, Judith
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John
;  APPLICANT:  Carr, Grant
;  APPLICANT:  Yamamoto, Robert
;  APPLICANT:  Forsyth, R.
;  APPLICANT:  Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31366
;   LENGTH: 3672
;   TYPE: DNA
;   ORGANISM: Pseudomonas putida
US-10-282-122A-31366

  Query Match             76.2%;  Score 16;  DB 13;  Length 3672;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGG 16
              ||||||||||||||||
Db       3545 GTGCCAGCAGCAGCGG 3560


RESULT 12
US-09-535-459-1477/c
; Sequence 1477, Application US/09535459
; Publication No. US20030040615A1
; GENERAL INFORMATION:
;  APPLICANT: Seilhamer, Jeffrey J.
;  APPLICANT:  Delegeane, Angelo M.
;  APPLICANT:  Stuart, Susan G.
;  APPLICANT:  Stuve, Laura L.
;  APPLICANT:  Mullahy, Sara J.
;  APPLICANT:  Naughton, Rebecca E.
;  TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE
;  FILE REFERENCE: PD-1014 CIP
;  CURRENT APPLICATION NUMBER: US/09/535,459
;  CURRENT FILING DATE:  2000-03-24
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 2170
;  SOFTWARE: PERL Program
; SEQ ID NO 1477
;   LENGTH: 280
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030040615A1 hu00988392
US-09-535-459-1477

  Query Match             71.4%;  Score 15;  DB 10;  Length 280;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GCCAGCAGCAGCGGT 17
              |||||||||||||||
Db        138 GCCAGCAGCAGCGGT 124


RESULT 13
US-09-535-459-1478/c
; Sequence 1478, Application US/09535459
; Publication No. US20030040615A1
; GENERAL INFORMATION:
;  APPLICANT: Seilhamer, Jeffrey J.
;  APPLICANT:  Delegeane, Angelo M.
;  APPLICANT:  Stuart, Susan G.
;  APPLICANT:  Stuve, Laura L.
;  APPLICANT:  Mullahy, Sara J.
```

```
;  APPLICANT:  Naughton, Rebecca E.
;  TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE
;  FILE REFERENCE: PD-1014 CIP
;  CURRENT APPLICATION NUMBER: US/09/535,459
;  CURRENT FILING DATE:  2000-03-24
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 2170
;  SOFTWARE: PERL Program
; SEQ ID NO 1478
;   LENGTH: 296
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030040615A1 hu01006476
US-09-535-459-1478

  Query Match             71.4%;  Score 15;  DB 10;  Length 296;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GCCAGCAGCAGCGGT 17
              ||||||||||||||||
Db        125 GCCAGCAGCAGCGGT 111


RESULT 14
US-09-535-459-1475/c
; Sequence 1475, Application US/09535459
; Publication No. US20030040615A1
; GENERAL INFORMATION:
;  APPLICANT: Seilhamer, Jeffrey J.
;  APPLICANT:  Delegeane, Angelo M.
;  APPLICANT:  Stuart, Susan G.
;  APPLICANT:  Stuve, Laura L.
;  APPLICANT:  Mullahy, Sara J.
;  APPLICANT:  Naughton, Rebecca E.
;  TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE
;  FILE REFERENCE: PD-1014 CIP
;  CURRENT APPLICATION NUMBER: US/09/535,459
;  CURRENT FILING DATE:  2000-03-24
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 2170
;  SOFTWARE: PERL Program
; SEQ ID NO 1475
;   LENGTH: 364
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030040615A1 hu01109550
US-09-535-459-1475

  Query Match             71.4%;  Score 15;  DB 10;  Length 364;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GCCAGCAGCAGCGGT 17
              ||||||||||||||||
Db        159 GCCAGCAGCAGCGGT 145


RESULT 15
US-09-535-459-1479/c
; Sequence 1479, Application US/09535459
; Publication No. US20030040615A1
; GENERAL INFORMATION:
;  APPLICANT: Seilhamer, Jeffrey J.
;  APPLICANT:  Delegeane, Angelo M.
;  APPLICANT:  Stuart, Susan G.
;  APPLICANT:  Stuve, Laura L.
;  APPLICANT:  Mullahy, Sara J.
;  APPLICANT:  Naughton, Rebecca E.
;  TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING ELECTRON TRANSFER MOLECULE
;  FILE REFERENCE: PD-1014 CIP
;  CURRENT APPLICATION NUMBER: US/09/535,459
;  CURRENT FILING DATE:  2000-03-24
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 2170
;  SOFTWARE: PERL Program
; SEQ ID NO 1479
;   LENGTH: 391
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030040615A1 hu01224429
US-09-535-459-1479

  Query Match             71.4%;  Score 15;  DB 10;  Length 391;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GCCAGCAGCAGCGGT 17
              ||||||||||||||||
Db        161 GCCAGCAGCAGCGGT 147


Search completed: August  4, 2004, 11:56:27
Job time : 191.012 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 04:00:30 ; Search time 172.554 Seconds
(without alignments)
517.009 Million cell updates/sec

Title: US-09-940-860-4
Perfect score: 21
Sequence: 1 gtgccagcagcagcggtaata 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	21	100.0	5849	2	AAV33135	Aav33135 Plasmodiu
c	2	17	81.0	1458	7	ABZ38180	Abz38180 N. gonorr
c	3	17	81.0	1542	2	AAZ12223	Aaz12223 Neisseria
	4	17	81.0	3593	4	ABL09563	Abl09563 Drosophil
	5	17	81.0	6161	4	ABL09562	Abl09562 Drosophil
	6	16	76.2	684	8	ADA31033	Ada31033 DNA encod
c	7	16	76.2	804	9	ADE63858	Ade63858 Rat gene
c	8	16	76.2	804	9	ADD48493	Add48493 Rat gene
	9	16	76.2	1119	7	ABT34135	Abt34135 Short het
	10	16	76.2	2854	4	ABL11243	Abl11243 Drosophil
	11	16	76.2	3672	7	ACA43496	Aca43496 Prokaryot
	12	16	76.2	5471	4	ABL11242	Abl11242 Drosophil
c	13	15	71.4	32	4	AAF60723	Aaf60723 Murine DL
	14	15	71.4	130	3	AAC61717	Aac61717 Clone VGT
c	15	15	71.4	197	9	ADD17780	Add17780 DNA (SeqI
c	16	15	71.4	336	4	ABL28181	Abl28181 Drosophil
c	17	15	71.4	571	7	ABZ73270	Abz73270 Rice leaf
c	18	15	71.4	640	9	ADD16180	Add16180 cDNA (Seq
c	19	15	71.4	716	9	ADD17056	Add17056 DNA (SeqI
	20	15	71.4	725	6	ABK31113	Abk31113 Plant dwa
c	21	15	71.4	908	7	ABT42347	Abt42347 Toxicity
c	22	15	71.4	1167	4	AAF81355	Aaf81355 Quorum se
	23	15	71.4	1167	4	ABL29451	Abl29451 Drosophil
c	24	15	71.4	1173	7	ACA45835	Aca45835 Prokaryot
c	25	15	71.4	1575	2	AAV02903	Aav02903 Human DNa
c	26	15	71.4	1636	3	AAA98876	Aaa98876 Human pro
c	27	15	71.4	1636	3	AAA98158	Aaa98158 Human pro
c	28	15	71.4	1636	6	AAD29987	Aad29987 Human pha
	29	15	71.4	1654	4	ABL17969	Abl17969 Drosophil
	30	15	71.4	1679	6	ABQ77568	Abq77568 Human ATP
c	31	15	71.4	1748	2	AAX22772	Aax22772 Human SOC
c	32	15	71.4	1748	2	AAX22778	Aax22778 Human SOC
c	33	15	71.4	1915	2	AAV29137	Aav29137 Homo sapi
	34	15	71.4	2039	7	ACC44418	Acc44418 Gene enco
c	35	15	71.4	2178	7	ACA47979	Aca47979 Prokaryot
c	36	15	71.4	2186	2	AAZ20095	Aaz20095 Cytokine
	37	15	71.4	2196	4	AAH17305	Aah17305 Human cDN
	38	15	71.4	2354	9	ADB63487	Adb63487 Human cDN
	39	15	71.4	2525	3	AAZ98625	Aaz98625 Silkworm
c	40	15	71.4	2558	2	AAZ20096	Aaz20096 Cytokine
c	41	15	71.4	2646	4	ABL07099	Abl07099 Drosophil
	42	15	71.4	2672	4	ABL28180	Abl28180 Drosophil
c	43	15	71.4	2860	6	ABT06279	Abt06279 Human NOV
c	44	15	71.4	2860	6	ABT06280	Abt06280 Human NOV
c	45	15	71.4	2924	9	ADD78281	Add78281 Human CGD

ALIGNMENTS

RESULT 1
AAV33135
ID AAV33135 standard; DNA; 5849 BP.
XX
AC AAV33135;
XX
DT 17-OCT-2003 (revised)
DT 07-DEC-1998 (first entry)
XX
DE Plasmodium berghei plastid PS1-PL470 gene.
XX
KW Malaria; infection; therapy; diagnosis; vaccine; plastid; PS1-PL470 gene;
KW ds.
XX
OS Plasmodium berghei; ANKA strain.
XX
PN WO9835057-A1.
XX
PD 13-AUG-1998.
XX
PF 05-FEB-1998; 98WO-IB000212.
XX
PR 06-FEB-1997; 97AU-00004953.
PR 21-APR-1997; 97AU-00006329.
PR 26-SEP-1997; 97AU-00009481.
XX
PA (UYSI-) UNIV SINGAPORE NAT.
PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.
XX
PI Kara AKU, Ting RCY, Tham JM, Nelson JS, Tan TMC;
XX
DR WPI; 1998-447251/38.
XX
PT Detecting Plasmodium infection from hybridisation with extrachromosomal
PT element - providing genus or species specific diagnosis with few false
PT negatives, in humans or animals.
XX
PS Claim 15; Page 54-59; 120pp; English.
XX
CC This is the nucleotide sequence of one strand of the PS1-PL470 gene of
CC the 30.7 kb extrachromosomal plastid of Plasmodium berghei. This plastid
CC encodes organelle-like rRNAs, tRNAs, ribosomal proteins and RNA
CC polymerase subunits, amongst others. Plasmodium is detected in a human or
CC animal sample by treating it, or derived nucleic acid, with a Plasmodium
CC extrachromosomal genetic element or derived nucleic acid (A) and
CC detecting any hybridisation. (A) can include the PS1-PL470, PLH-PPH, PRB

CC or PWQ gene, the mitochondrial coxI gene, and nucleic acids derived from
CC them. Also new are (A)-specific probes and primers (see AAV33139-56). The
CC method is used to diagnose Plasmodium infection. Also (not claimed) the
CC polypeptides encoded by (A) are useful as targets for drug development
CC and for development of anti-malaria vaccines. The high degree of
CC similarity between (A) from different species allows development of genus
CC - or species-specific assays that result in fewer false negatives than
CC known methods (typically 1% against 3%). (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 5849 BP; 2296 A; 673 C; 557 G; 2323 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 2; Length 5849;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGGTAATA 21
||||||||||||||||||||||
Db 4671 GTGCCAGCAGCAGCGGTAATA 4691

RESULT 2
ABZ38180/c
ID ABZ38180 standard; DNA; 1458 BP.
XX
AC ABZ38180;
XX
DT 07-MAR-2003 (first entry)
XX
DE N. gonorrhoeae nucleotide sequence SEQ ID 949.
XX
KW Antibacterial; infection; vaccine; gene therapy; gene; ds.
XX
OS Neisseria gonorrhoeae.
XX
PN WO200279243-A2.
XX
PD 10-OCT-2002.
XX
PF 12-FEB-2002; 2002WO-IB002069.
XX
PR 12-FEB-2001; 2001GB-00003424.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Fontana MR, Pizza M, Masignani V, Monaci E;
XX
DR WPI; 2003-058415/05.
DR P-PSDB; ABP77210.
XX
PT New protein from Neisseria gonorrheae, useful for the manufacture of a
PT medicament for treating or preventing N. gonorrheae infection.
XX
PS Disclosure; Page 257; 815pp; English.
XX
CC The present invention relates to proteins from Neisseria gonorrhoeae.
CC Also disclosed are the nucleic acid molecules encoding the proteins and
CC antibodies that specifically bind to the proteins. The composition
CC comprising the protein, nucleic acid or antibody is useful for the
CC manufacture of a medicament for treating or preventing N. gonorrhoeae
CC infection, this may be in the form of a vaccine or gene therapy.
CC Sequences given in records ABZ37706-ABZ42016 represent nucleic acid
CC molecules of the invention
XX
SQ Sequence 1458 BP; 167 A; 328 C; 569 G; 394 T; 0 U; 0 Other;

Query Match 81.0%; Score 17; DB 7; Length 1458;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCCAGCAGCAGCGGTAA 19
|||||||||||||||||
Db 1067 GCCAGCAGCAGCGGTAA 1051

RESULT 3
AAZ12223/c
ID AAZ12223 standard; DNA; 1542 BP.
XX
AC AAZ12223;
XX
DT 08-OCT-1999 (first entry)
XX
DE Neisseria gonorrhoeae complete ORF139 sequence.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW treatment; Neisseria infection; meningitis; septicaemia; gonorrhea; ss.
XX
OS Neisseria gonorrhoeae.
XX
PN WO9924578-A2.
XX
PD 20-MAY-1999.
XX
PF 09-OCT-1998; 98WO-IB001665.
XX
PR 06-NOV-1997; 97GB-00023516.
PR 14-NOV-1997; 97GB-00024190.
PR 18-NOV-1997; 97GB-00024386.
PR 27-NOV-1997; 97GB-00025158.
PR 10-DEC-1997; 97GB-00026147.
PR 14-JAN-1998; 98GB-00000759.
PR 01-SEP-1998; 98GB-00019016.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Masignani V, Rappuoli R, Pizza M, Scarlato V, Grandi G;
XX
DR WPI; 1999-327407/27.
DR N-PSDB; AAZ12223.
XX
PT Proteins from Neisseria meningitidis and N. gonorrhoeae useful for
PT diagnosis, treatment and prevention of infection.
XX
PS Claim 9; Page 332; 524pp; English.
XX
CC Nucleotide sequences AAZ11972-Z12358 represent open reading frames (ORFs)
CC of Neisseria meningitidis and N. gonorrhoeae which encode antigenic
CC proteins (see AAY38499-Y38944). The antigenic proteins, their fragments,
CC their nucleic acids and antibodies are used for diagnosis, prevention (as
CC vaccines) or treatment of Neisseria infections, such as meningitis,
CC septicaemia and gonorrhea. Both organisms are closely related. Fragments
CC of the nucleic acids are useful as hybridisation probes and antisense
CC reagents
XX
SQ Sequence 1542 BP; 175 A; 345 C; 599 G; 423 T; 0 U; 0 Other;

Query Match 81.0%; Score 17; DB 2; Length 1542;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCCAGCAGCAGCGGTAA 19
|||||||||||||||||
Db 1148 GCCAGCAGCAGCGGTAA 1132

RESULT 4
ABL09563
ID ABL09563 standard; cDNA; 3593 BP.
XX
AC ABL09563;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 23171.
XX

KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB65460.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Claim 1; SEQ ID NO 23171; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3593 BP; 1055 A; 1047 C; 919 G; 572 T; 0 U; 0 Other;

Query Match 81.0%; Score 17; DB 4; Length 3593;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGCCAGCAGCAGCGGTA 18
||||||||||||||||||
Db 3467 TGCCAGCAGCAGCGGTA 3483

RESULT 5
ABL09562
ID ABL09562 standard; cDNA; 6161 BP.
XX
AC ABL09562;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 23168.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB65459.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Claim 1; SEQ ID NO 23168; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 6161 BP; 1747 A; 1568 C; 1438 G; 1408 T; 0 U; 0 Other;

Query Match 81.0%; Score 17; DB 4; Length 6161;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGCCAGCAGCAGCGGTA 18
||||||||||||||||||
Db 5035 TGCCAGCAGCAGCGGTA 5051

RESULT 6
ADA31033
ID ADA31033 standard; DNA; 684 BP.
XX
AC ADA31033;
XX
DT 20-NOV-2003 (first entry)
XX
DE DNA encoding Acinetobacter baumannii protein #2320.
XX
KW ds; gene; Acinetobacter baumannii; bacterial disease; antibacterial;
KW vaccine; plant biocontrol agent.
XX
OS Acinetobacter baumannii.
XX
PN US6562958-B1.
XX
PD 13-MAY-2003.
XX
PF 04-JUN-1999; 99US-00328352.
XX
PR 09-JUN-1998; 98US-0088701P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Breton G, Bush D;
XX
DR WPI; 2003-576092/54.
DR P-PSDB; ADA35159.
XX
PT New Acinetobacter baumanii proteins and nucleic acids, useful as reagents
PT for diagnosing a bacterial disease, as components of antibacterial
PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for
PT plants.
XX
PS Example; SEQ ID NO 2320; 328pp; English.
XX
CC The invention relates to isolated Acinetobacter baumannii nucleic acids.

CC The A. baumannii nucleic acids and polypeptides are useful as reagents
CC for diagnosing a bacterial disease, as components of antibacterial
CC vaccines, as targets for antibacterial drugs, to detect the presence of
CC A. baumannii and other Acinetobacter species in a sample, in screening
CC compounds for the ability to interfere with the A. baumannii life cycle
CC or to inhibit A. baumannii infection, and as biocontrol agents for
CC plants. The present sequence represents DNA encoding an A. baumannii
CC protein.
XX
SQ Sequence 684 BP; 203 A; 127 C; 159 G; 195 T; 0 U; 0 Other;

Query Match 76.2%; Score 16; DB 8; Length 684;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGCAGCAGCGGTAAT 20
||||||||||||||||
Db 170 CAGCAGCAGCGGTAAT 185

RESULT 7
ADE63858/c
ID ADE63858 standard; DNA; 804 BP.
XX
AC ADE63858;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat gene X62660, SEQ ID NO 9802.
XX
KW Rat; ds; gene; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; X62660.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat DNA (shown in Table 2 of the
CC specification) which is differentially expressed during pain. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 804 BP; 261 A; 178 C; 198 G; 167 T; 0 U; 0 Other;

Query Match 76.2%; Score 16; DB 9; Length 804;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGG 16
||||||||||||||||
Db 92 GTGCCAGCAGCAGCGG 77

RESULT 8
ADD48493/c
ID ADD48493 standard; DNA; 804 BP.
XX
AC ADD48493;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat gene X62660, SEQ ID NO 14194.
XX
KW Rat; ds; gene; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; X62660.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal

CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat DNA (shown in Table 2 of the
CC specification) which encodes one of the polypeptides of the invention
CC which is differentially expressed during pain. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 804 BP; 261 A; 178 C; 198 G; 167 T; 0 U; 0 Other;

Query Match 76.2%; Score 16; DB 9; Length 804;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGG 16
||||||||||||||||
Db 92 GTGCCAGCAGCAGCGG 77

RESULT 9
ABT34135
ID ABT34135 standard; DNA; 1119 BP.
XX
AC ABT34135;
XX
DT 12-JUN-2003 (first entry)
XX
DE Short heterodimer partner-1 expression mouse DNA SEQ ID No 10.
XX
KW Antiarteriosclerotic; cardiant; vasotropic; antiinfective; cytostatic;
KW antiinflammatory; inhibitor; antisense gene therapy; atherosclerosis;
KW short heterodimer partner-1; abnormal; lipid; cholesterol metabolism;
KW cardiovascular disease; infection; inflammation; tumour formation; mouse;
KW murine; ds.
XX
OS Mus musculus.
XX
PN WO2003012033-A2.
XX
PD 13-FEB-2003.
XX
PF 17-JUL-2002; 2002WO-US023245.
XX
PR 31-JUL-2001; 2001US-00919197.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Crooke RM, Graham MJ;
XX
DR WPI; 2003-248161/24.
DR P-PSDB; AAO27109.
XX
PT New antisense oligonucleotide targeted to a nucleic acid encoding short
PT heterodimer partner-1, useful for treating diseases involving abnormal
PT lipid or cholesterol metabolism, e.g atherosclerosis or cardiovascular
PT diseases.
XX
PS Example 9; Page 103-105; 121pp; English.
XX
CC The invention relates to a novel compound of 8 - 50 nucleobases in length
CC targeted to a nucleic acid molecule encoding a short heterodimer partner-
CC 1. The novel compound specifically hybridizes with a nucleic acid
CC molecule encoding the short heterodimer partner-1, and inhibits the
CC expression of the nucleic acid molecule. The compound, and a composition
CC comprising it are useful for treating a disease or condition associated
CC with the short heterodimer partner-1, particularly a condition involving
CC abnormal lipid or cholesterol metabolism such as atherosclerosis or a
CC cardiovascular disease. They are also useful in research and diagnostics
CC for modulating the expression of short heterodimer partner-1. They can
CC also be useful prophylactically in preventing or delaying infection,
CC inflammation or tumour formation. This polynucleotide represents a mouse
CC DNA sequence relating to the short heterodimer partner-1 of the invention
XX
SQ Sequence 1119 BP; 233 A; 354 C; 289 G; 243 T; 0 U; 0 Other;

Query Match 76.2%; Score 16; DB 7; Length 1119;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGG 16
||||||||||||||||
Db 161 GTGCCAGCAGCAGCGG 176

RESULT 10
ABL11243
ID ABL11243 standard; cDNA; 2854 BP.
XX
AC ABL11243;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 28211.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB67140.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Claim 1; SEQ ID NO 28211; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2854 BP; 775 A; 789 C; 705 G; 585 T; 0 U; 0 Other;

```
  Query Match             76.2%;  Score 16;  DB 4;  Length 2854;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CCAGCAGCAGCGGTAA 19
              ||||||||||||||||
Db       2354 CCAGCAGCAGCGGTAA 2369


RESULT 11
ACA43496
ID   ACA43496 standard; DNA; 3672 BP.
XX
AC   ACA43496;
XX
DT   19-JUN-2003  (first entry)
XX
DE   Prokaryotic essential gene #25153.
XX
KW   Antisense; ds; prokaryotic essential gene; cell proliferation;
KW   drug design; gene.
XX
OS   Pseudomonas putida.
XX
PN   WO200277183-A2.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2002; 2002WO-US009107.
XX
PR   21-MAR-2001; 2001US-00815242.
PR   06-SEP-2001; 2001US-00948993.
PR   25-OCT-2001; 2001US-0342923P.
PR   08-FEB-2002; 2002US-00072851.
PR   06-MAR-2002; 2002US-0362699P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Wang L,  Zamudio C,  Malone C,  Haselbeck R,  Ohlsen KL,  Zyskind JW;
PI   Wall D,  Trawick JD,  Carr GJ,  Yamamoto R,  Forsyth RA,  Xu HH;
XX
DR   WPI; 2003-029926/02.
DR   P-PSDB; ABU39626.
XX
PT   New antisense nucleic acids, useful for identifying proteins or screening
PT   for homologous nucleic acids required for cellular proliferation to
PT   isolate candidate molecules for rational drug discovery programs.
XX
PS   Claim 14; SEQ ID NO 31366; 1766pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising any one of
CC   the 6213 antisense sequences given in the specification where expression
CC   of the nucleic acid inhibits proliferation of a cell. Also included are:
CC   (1) a vector comprising a promoter operably linked to the nucleic acid
CC   encoding a polypeptide whose expression is inhibited by the antisense
CC   nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC   polypeptide or its fragment whose expression is inhibited by the
CC   antisense nucleic acid; (4) an antibody capable of specifically binding
CC   the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC   proliferation or the activity of a gene in an operon required for
CC   proliferation; (7) identifying a compound that influences the activity of
CC   the gene product or that has an activity against a biological pathway
CC   required for proliferation, or that inhibits cellular proliferation; (8)
CC   identifying a gene required for cellular proliferation or the biological
CC   pathway in which a proliferation-required gene or its gene product lies
CC   or a gene on which the test compound that inhibits proliferation of an
CC   organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC   compound's activity; (11) a culture comprising strains in which the gene
CC   product is overexpressed or underexpressed; (12) determining the extent
CC   to which each of the strains is present in a culture or collection of
CC   strains; or (13) identifying the target of a compound that inhibits the
CC   proliferation of an organism. The antisense nucleic acids are useful for
CC   identifying proteins or screening for homologous nucleic acids required
CC   for cellular proliferation to isolate candidate molecules for rational
CC   drug discovery programs, or for screening homologous nucleic acids
CC   required for proliferation in cells other than S. aureus, S. typhimurium,
CC   K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC   prokaryotic essential genes. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 3672 BP; 660 A; 1207 C; 1179 G; 626 T; 0 U; 0 Other;

  Query Match             76.2%;  Score 16;  DB 7;  Length 3672;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGG 16
              ||||||||||||||||
Db       3545 GTGCCAGCAGCAGCGG 3560


RESULT 12
ABL11242
ID   ABL11242 standard; cDNA; 5471 BP.
XX
AC   ABL11242;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 28208.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ss.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US009231.
XX
PR   23-MAR-2000; 2000US-0191637P.
PR   11-JUL-2000; 2000US-00614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   P-PSDB; ABB67139.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signaling and cell-cell
PT   interactions.
XX
PS   Claim 1; SEQ ID NO 28208; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC   ABB72072). The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 5471 BP; 1481 A; 1326 C; 1238 G; 1426 T; 0 U; 0 Other;

  Query Match             76.2%;  Score 16;  DB 4;  Length 5471;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

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Qy          4 CCAGCAGCAGCGGTAA 19
              ||||||||||||||||
Db       3971 CCAGCAGCAGCGGTAA 3986
```

RESULT 13
AAF60723/c
ID AAF60723 standard; DNA; 32 BP.
XX
AC AAF60723;
XX
DT 03-MAY-2001 (first entry)
XX
DE Murine DLAD signal peptide PCR primer #1.
XX
KW Murine; DNase; DLAD; deoxyribonuclease; endonuclease; cystic fibrosis;
KW infectious disease; PCR primer; ss.
XX
OS Mus musculus.
XX
PN WO200112793-A1.
XX
PD 22-FEB-2001.
XX
PF 01-MAY-2000; 2000WO-JP002893.
XX
PR 17-AUG-1999; 99JP-00230870.
XX
PA (TANU/) TANUMA S.
XX
PI Tanuma S, Shiokawa D;
XX
DR WPI; 2001-218348/22.
XX
PT Acidic deoxyribonuclease capable of divalent cation-independent cleavage
PT of DNA under acidic even neutral pH and not inhibited by G-actin, useful
PT in remedies for cystic fibrosis and for treatment of infectious diseases.
XX
PS Example 3; Page 29; 61pp; Japanese.
XX
CC The present invention relates to deoxyribonuclease (DLAD) proteins and
CC coding sequences, (see AAF60715-6 and AAB72416-7). DLAD is an
CC endonuclease and is capable of divalent cation-independent cleavage of
CC DNA under acidic conditions. DLAD can be used as a substitute for DNase I
CC in treating cystic fibrosis, and is useful in the prevention and
CC treatment of infectious diseases. The present sequence is a PCR primer
CC for murine DLAD signal peptide (AAF60715)
XX
SQ Sequence 32 BP; 5 A; 13 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 71.4%; Score 15; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 TGCCAGCAGCAGCGG 16
              |||||||||||||||
Db         32 TGCCAGCAGCAGCGG 18
```

RESULT 14
AAC61717
ID AAC61717 standard; DNA; 130 BP.
XX
AC AAC61717;
XX
DT 15-SEP-2003 (revised)
DT 06-MAR-2001 (first entry)
XX
DE Clone VGT18 of a gene that is differentially regulated by viral Jun.
XX
KW Viral Jun; v-Jun; cellular Jun; c-Jun; immune system disorder;
KW haematopoietic cell disorder; autoimmune disorder; allergy; inflammation;
KW organ rejection; graft-versus-host-disease; hyperproliferative disorder;
KW infection; food additive; storage capability; nutritional component; ss.
XX
OS Gallus gallus.
XX
PN WO200061738-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009766.
XX
PR 12-APR-1999; 99US-0128887P.
XX
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI Vogt PK, Fu S, Hilbush BS, Bottoli ILC, Dickerson JC;
XX
DR WPI; 2000-628402/60.
XX
PT Isolated nucleic acid molecules from Gallus domesticus are used for
PT diagnosis and treatment of medial conditions in mammals e.g. cancers.
XX
PS Claim 3; Page 92; 99pp; English.
XX
CC The present sequence is derived from a gene that is differentially
CC regulated by viral Jun (v-Jun) and cellular Jun (c-Jun). The
CC polynucleotide is used to prevent, treat or ameliorate a medical
CC condition, e.g. deficiencies or disorders of the immune system, of
CC haematopoietic cells, autoimmune disorders, allergic conditions, organ
CC rejection or graft-versus-host-disease, inflammation, hyperproliferative
CC disorders, bacterial, fungal, parasitic and virus infections. It can also
CC be used to modulate hemostatic or thrombolytic activity, regenerate
CC tissues, increase chemotaxic activity of cells, modulate mammalian
CC metabolism, change the physical or mental state of a mammal and can be
CC used as food additives to increase or decrease storage capabilities and
CC nutritional components. (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ Sequence 130 BP; 40 A; 37 C; 30 G; 23 T; 0 U; 0 Other;

Query Match 71.4%; Score 15; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GTGCCAGCAGCAGCG 15
              |||||||||||||||
Db         51 GTGCCAGCAGCAGCG 65
```

RESULT 15
ADD17780/c
ID ADD17780 standard; DNA; 197 BP.
XX
AC ADD17780;
XX
DT 15-JAN-2004 (first entry)
XX
DE DNA (SeqID 1848) that confers an altered visual phenotype in plants.
XX
KW ds; visual phenotype; plant; architecture; leaf surface; chlorotic;
KW bleaching; etching; wet leaf; stunting; elongation; texture;
KW agronomic trait; growth regulation; dwarf variety; insect resistance;
KW heat stress; transgenic.
XX
OS Unidentified.
XX
PN WO2003020741-A1.
XX
PD 13-MAR-2003.
XX
PF 30-AUG-2002; 2002WO-US027880.
XX
PR 31-AUG-2001; 2001US-0316326P.
XX

PA (DOWC) DOW CHEM CO.
PA (DOWC) DOW AGROSCIENCES LLC.
XX
PI Crosley R, Skokut T, Ruegger M, Larrinua I, Shukla V;
XX
DR WPI; 2003-300858/29.
XX
PT Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae
PT sativa, Saccharomyces cerevisiae, and Papaver rhoeas, useful for
PT conferring altered visual phenotypes in plants.
XX
PS Claim 1; SEQ ID NO 1848; 517pp; English.
XX
CC This invention relates to the identification and isolation of novel
CC nucleic acid molecules that confer altered visual phenotypes in plants.
CC Specifically, it refers to modifications of plant architecture and/ or
CC leaf surface features in plants, such as chlorotic, bleaching, etching,
CC wet leaf, stunting, elongation and texture phenotypes, which are thought
CC will be agronomic traits beneficial to the farmer. As such, these novel
CC phenotypes can affect growth regulation i.e. useful for creating dwarf
CC varieties, exhibit resistance to insects or heat stress, confer changes
CC in pigment content such that plants have enhanced vitamin production or
CC delayed senescence and also for example produce plants that control the
CC production of ethylene. Furthermore, the present invention comprises
CC generating transgenic plants, as well as reproducibly altering the visual
CC phenotype of plant seeds, plant tissues and plant cells containing the
CC polynucleotides described herein. This polynucleotide is a homologue of a
CC DNA sequence that confers an altered visual phenotype when expressed in
CC plants, the method of the invention.
XX
SQ Sequence 197 BP; 46 A; 66 C; 42 G; 43 T; 0 U; 0 Other;

Query Match 71.4%; Score 15; DB 9; Length 197;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 GCCAGCAGCAGCGGT 17
              |||||||||||||||
Db         74 GCCAGCAGCAGCGGT 60
```

Search completed: August 4, 2004, 06:43:39
Job time : 174.554 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 05:41:25 ; Search time 1462.92 Seconds
(without alignments)
428.668 Million cell updates/sec

Title: US-09-940-860-4
Perfect score: 21
Sequence: 1 gtgccagcagcagcggtaata 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	21	100.0	420	14	CD087130	CD087130 MC1-0035T
	2	21	100.0	1128	29	CG745724	CG745724 P038-3-H1
c	3	20	95.2	316	12	BI936798	BI936798 dc89d01.x
c	4	20	95.2	418	10	BE517377	BE517377 WHE0625_B
c	5	18	85.7	915	28	AZ677920	AZ677920 ENTHX83TR
c	6	17	81.0	73	14	CB832595	CB832595 SWWbmfCAV
	7	17	81.0	148	9	AU010207	AU010207 AU010207
	8	17	81.0	252	14	CK107208	CK107208 UB49DPG02
c	9	17	81.0	413	9	AU007074	AU007074 AU007074
c	10	17	81.0	460	12	BG632306	BG632306 GH06375.3
c	11	17	81.0	475	9	AA695154	AA695154 GM02326.3
c	12	17	81.0	524	10	AW940266	AW940266 GH07623.3
c	13	17	81.0	540	9	AI518472	AI518472 LD37996.3
c	14	17	81.0	554	10	BF331275	BF331275 RC5-BT037
c	15	17	81.0	619	9	AI397756	AI397756 NCC5H8T3
	16	17	81.0	643	14	CD865408	CD865408 AZO2.073O
	17	17	81.0	707	14	CD873121	CD873121 AZO2.122G
	18	17	81.0	724	12	BM584191	BM584191 170006872
	19	17	81.0	745	29	CC539904	CC539904 CH240_420
c	20	17	81.0	750	28	AZ124708	AZ124708 OSJNBb007
	21	17	81.0	774	29	CC849995	CC849995 NDL.121H1
c	22	17	81.0	791	28	AQ914844	AQ914844 nbeb0049P
	23	17	81.0	842	14	CK203195	CK203195 FGAS01172
	24	17	81.0	865	14	CK203537	CK203537 FGAS01206
c	25	17	81.0	886	14	CA581282	CA581282 EST000957
c	26	17	81.0	933	14	CA583063	CA583063 EST002738
	27	17	81.0	1101	29	CNS00ZBC	AL097458 Drosophil
	28	17	81.0	1163	13	BU598465	BU598465 AGENCOURT
c	29	16	76.2	186	28	AZ269457	AZ269457 RPCI-23-4
c	30	16	76.2	222	10	BB589921	BB589921 BB589921
c	31	16	76.2	225	10	BB604685	BB604685 BB604685
c	32	16	76.2	277	10	AW866950	AW866950 CM3-SN003
	33	16	76.2	278	13	BU648979	BU648979 1112075A1
c	34	16	76.2	336	9	AJ281902	AJ281902 4A3A-AAM-
c	35	16	76.2	337	13	BY326251	BY326251 BY326251
c	36	16	76.2	337	13	BY775272	BY775272 BY775272
c	37	16	76.2	338	13	BY275520	BY275520 BY275520
	38	16	76.2	355	12	BI138225	BI138225 F101P50Y
c	39	16	76.2	355	13	BY318904	BY318904 BY318904
	40	16	76.2	359	9	AA670731	AA670731 vp87c05.r
c	41	16	76.2	370	13	BY769530	BY769530 BY769530
c	42	16	76.2	370	29	BX218719	BX218719 Danio rer
c	43	16	76.2	373	13	BY012711	BY012711 BY012711
c	44	16	76.2	374	28	BH677479	BH677479 BOMCU92TF
c	45	16	76.2	376	13	BY769221	BY769221 BY769221

ALIGNMENTS

RESULT 1
CD087130/c
LOCUS CD087130 420 bp mRNA linear EST 14-SEP-2003
DEFINITION MC1-0035T-R100-D10-U.G MC1-0035 Schistosoma mansoni cDNA clone MC1-0035T-R100-D10.G, mRNA sequence.
ACCESSION CD087130
VERSION CD087130.1 GI:34638055
KEYWORDS EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE 1 (bases 1 to 420)
AUTHORS Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M., Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr., Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F., Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L., Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A., Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A., Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T., Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M., Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
TITLE Transcriptome analysis of the acoelomate human parasite Schistosoma mansoni
JOURNAL Nat. Genet. 35 (2), 148-157 (2003)
MEDLINE 22879926
COMMENT Contact: Dr. Sergio Verjovski-Almeida

Departamento de Bioquimica
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP, Brasil
Tel: +55-11-3091-2173
Fax: +55-11-3091-2186
Email: verjo@iq.usp.br
This sequence was derived from the FAPESP Schistosoma mansoni EST Genome Project. All sequences in the project were assembled and annotated. This entry and all the assembled sequences can be seen in the following URL http://bioinfo.iq.usp.br/schisto/
Plate: MC1-0035T-R100 row: 10 column: D.

FEATURES Location/Qualifiers
source 1. .420
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="MC1-0035T-R100-D10.G"
/sex="mixed pool"
/dev_stage="cercaria"
/lab_host="Biomphalaria glabrata"
/clone_lib="MC1-0035"
/note="Vector: pGEM T-easy"

ORIGIN

Query Match 100.0%; Score 21; DB 14; Length 420;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGGTAATA 21
||||||||||||||||||||
Db 31 GTGCCAGCAGCAGCGGTAATA 11

RESULT 2
CG745724
LOCUS CG745724 1128 bp DNA linear GSS 24-OCT-2003
DEFINITION P038-3-H12.ya Ppa EcoRI BAC Library Pristionchus pacificus genomic, genomic survey sequence.
ACCESSION CG745724
VERSION CG745724.1 GI:37966650
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 1128)
AUTHORS Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K., Buntjer,J., van der Meulen,M. and Sommer,R.J.
TITLE An integrated physical and genetic map of the nematode Pristionchus pacificus
JOURNAL Mol. Genet. Genomics 269 (5), 715-722 (2003)
MEDLINE 22835951
PUBMED 12884007
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
FEATURES Location/Qualifiers
source 1. .1128
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC vector."

ORIGIN

Query Match 100.0%; Score 21; DB 29; Length 1128;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGGTAATA 21
||||||||||||||||||||
Db 477 GTGCCAGCAGCAGCGGTAATA 497

RESULT 3
BI936798/c
LOCUS BI936798 316 bp mRNA linear EST 18-OCT-2001
DEFINITION dc89d01.x1 NICHD_XGC_OO1 Xenopus laevis cDNA clone IMAGE:3404257 3' similar to TR:O14597 O14597 NON-FUNCTIONAL FOLATE BINDING PROTEIN. ;, mRNA sequence.
ACCESSION BI936798
VERSION BI936798.1 GI:16251270
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 316)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .316
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:3404257"
/tissue_type="oocytes"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD_XGC_OO1"
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.2 kb. Constructed by Life Technologies."
ORIGIN

Query Match 95.2%; Score 20; DB 12; Length 316;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGGTAAT 20
||||||||||||||||||||
Db 299 GTGCCAGCAGCAGCGGTAAT 280

RESULT 4
BE517377/c
LOCUS BE517377 418 bp mRNA linear EST 08-AUG-2000
DEFINITION WHE0625_B06_C11ZA Wheat ABA-treated embryo cDNA library Triticum aestivum cDNA clone WHE0625_B06_C11, mRNA sequence.
ACCESSION BE517377
VERSION BE517377.1 GI:9741407
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)

```
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 418)
  AUTHORS   Anderson,O.D., Chao,S., Han,P.S., Hsia,C.C., Johnson,R.R, Kang,Y.,
            Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L., Tong,J.C.,
            Verhey,S.D. and Walker-Simmons,M.K.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - ABA-treated embryo library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Clontech Matchmaker 3' AD primer.
FEATURES             Location/Qualifiers
     source          1. .418
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /cultivar="Brevor (soft, white, winter, common wheat)"
                     /db_xref="taxon:4565"
                     /clone="WHE0625_B06_C11"
                     /tissue_type="Seed embryo"
                     /dev_stage="Mature dormant seeds"
                     /lab_host="E. coli DH12S"
                     /clone_lib="Wheat ABA-treated embryo cDNA library"
                     /note="Vector: pGAD10; Site_1: EcoRI; Site_2: XhoI;
                     Embryos were cut from mature, dormant seeds and imbibed in
                     25 microM ABA  (abscisic acid) in 5 mM Mes buffer, pH 5.7,
                     for 12 hr at 22 C.  The  tissue, total RNA, and poly(A)
                     RNA were prepared by Steven Verhey in  M.K.
                     Walker-Simmons's lab (USDA-ARS, Washington State Univ.,
                     Pullman,  Washington 99164-6420.  A cDNA library was made
                     by Clontech using a  combination of random and oligo dT
                     primers. Library was plated and  archived by Russell
                     Johnson (Colby College, ME/Walker-Simmons' lab).  Plasmid
                     DNA preparations and DNA sequencing were performed in the
                     OD  Anderson lab (all other authors)."
ORIGIN

  Query Match             95.2%;  Score 20;  DB 10;  Length 418;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAAT 20
              ||||||||||||||||||||
Db        304 GTGCCAGCAGCAGCGGTAAT 285


RESULT 5
AZ677920/c
LOCUS       AZ677920                915 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  ENTHX83TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
            genomic, genomic survey sequence.
ACCESSION   AZ677920
VERSION     AZ677920.1  GI:11815186
KEYWORDS    GSS.
SOURCE      Entamoeba histolytica
  ORGANISM  Entamoeba histolytica
            Eukaryota; Entamoebidae; Entamoeba.
REFERENCE   1  (bases 1 to 915)
  AUTHORS   Loftus,B., Van Aken,S. and Fraser,C.
  TITLE     Determination of clone end sequences from Entamoeba histolytica
            HM1:IMSS sheared DNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Brendan J Loftus
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0208
            Fax: 301 838 3543
            Email: bjloftus@tigr.org
            Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
            DNA library
            Seq primer: M13-Reverse
            Class: shotgun
            High quality sequence start: 176
            High quality sequence stop: 283.
FEATURES             Location/Qualifiers
     source          1. .915
                     /organism="Entamoeba histolytica"
                     /mol_type="genomic DNA"
                     /strain="HM1:IMSS"
                     /db_xref="taxon:5759"
                     /clone_lib="Entamoeba histolytica Sheared DNA"
                     /note="Vector: pHOS1; Site_1: Bst I; Constructed at The
                     Institute for Genomic Research (TIGR), Rockville, MD.
                     Genomic DNA isolated from broth cultures of E. histolytica
                     using a  method described by Clark and Diamond (Clark,
                     C.G., and Diamond, L.S.  (1993) Entamoeba histolytica: a
                     method for isolate identification.  Exp. Parasitol.
                     77:450.). The DNA was mechanically sheared to give a
                     tight size distribution (~2 kb). The v + i method used for
                     the library  construction is described in detail in Smith,
                     H.O. and Venter, J.C.  (Making small insert libraries for
                     whole genome shotgun sequencing  projects. In Genome
                     Sequencing: A Practical Approach, eds. M. Vaudin  and B.
                     Barell, Oxford University Press, 1999)."
ORIGIN

  Query Match             85.7%;  Score 18;  DB 28;  Length 915;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GCCAGCAGCAGCGGTAAT 20
              ||||||||||||||||||
Db        891 GCCAGCAGCAGCGGTAAT 874


RESULT 6
CB832595/c
LOCUS       CB832595                  73 bp    mRNA    linear   EST 21-APR-2003
DEFINITION  SWWbmfCAV08B01SK Wuchereria bancrofti microfilaria cDNA
            (SAW95SjL-WbMf) Wuchereria bancrofti cDNA clone SWWbmfCAV08B01 5',
            mRNA sequence.
ACCESSION   CB832595
VERSION     CB832595.1  GI:30030842
KEYWORDS    EST.
SOURCE      Wuchereria bancrofti
  ORGANISM  Wuchereria bancrofti
            Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
            Onchocercidae; Wuchereria.
REFERENCE   1  (bases 1 to 73)
  AUTHORS   Williams,S.A.
  TITLE     Genes expressed in microfilaria of Wuchereria bancrofti
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Steven A. Williams
            Molecular Parasitology
            Smith College Department of Biological Sciences
            Department of Biological Sciences, Clark Science Center, Smith
            College, Northampton, MA, 01063, USA
            Tel: 4135853826
            Fax: 4135853786
            Email: genome@smith.edu
            Seq primer: pBluescript SK.
FEATURES             Location/Qualifiers
     source          1. .73
                     /organism="Wuchereria bancrofti"
                     /mol_type="mRNA"
                     /db_xref="taxon:6293"
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/clone="SWWbmfCAV08B01"
/dev_stage="microfilaria"
/lab_host="XL1-Blue MRF'"
/clone_lib="Wuchereria bancrofti microfilaria cDNA (SAW95SjL-WbMf)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from approximately 85,000 microfilariae isolated from the blood of an infected individual from Guyana, South America and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 2.9 x 10E5 independent recombinants and the average insert size is ~1kb. The library was constructed by Sandra J. Laney. The library is available from Dr.S.A.Williams, email: genome@smith.edu."

ORIGIN

Query Match 81.0%; Score 17; DB 14; Length 73;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGCAGCAGCGGTAATA 21
||||||||||||||||||
Db 37 CAGCAGCAGCGGTAATA 21

RESULT 7
AU010207
LOCUS AU010207 148 bp mRNA linear EST 31-JUL-1998
DEFINITION AU010207 Schizosaccharomyces pombe late log phase cDNA Schizosaccharomyces pombe cDNA clone spc05561, mRNA sequence.
ACCESSION AU010207
VERSION AU010207.1 GI:3346887
KEYWORDS EST.
SOURCE Schizosaccharomyces pombe (fission yeast)
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE 1 (bases 1 to 148)
AUTHORS Morimyo,M. and Mita,K.
TITLE Identification of expressed sequence tags of Schizosaccharomyces pombe
JOURNAL Unpublished (1998)
COMMENT Contact: Mitsuoki Morimyo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
FEATURES Location/Qualifiers
source 1. .148
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"
/clone="spc05561"
/sex="h minus"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"

ORIGIN

Query Match 81.0%; Score 17; DB 9; Length 148;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGGT 17
|||||||||||||||||
Db 68 GTGCCAGCAGCAGCGGT 84

RESULT 8
CK107208
LOCUS CK107208 252 bp mRNA linear EST 01-DEC-2003
DEFINITION UB49DPG02.5pR Populus active cambium cDNA library Populus tremula cDNA clone UB49DPG02 5', mRNA sequence.
ACCESSION CK107208
VERSION CK107208.1 GI:38591533
KEYWORDS EST.
SOURCE Populus tremula
ORGANISM Populus tremula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
REFERENCE 1 (bases 1 to 252)
AUTHORS Sterky,F., Bhalerao,R.R., Unneberg,P., Segerman,B., Nilsson,P., Brunner,A.M., Campaa,L., Jonsson-Lindvall,J., Tandre,K., Strauss,S.H., Sundberg,B., Gustafsson,P., Uhlen,M., Bhalerao,R.P., Nilsson,O., Sandberg,G., Karlsson,J., Lundeberg,J. and Jansson,S.
TITLE A Populus EST resource for functional genomics
JOURNAL Unpublished (2003)
COMMENT Other_ESTs: UB49DPG02, UB49DPG02.3pR
Contact: Bo Segerman
Umea Plant Science Center, Department of Plant Physiology
Umea University
901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: bo.segerman@plantphys.umu.se.
FEATURES Location/Qualifiers
source 1. .252
/organism="Populus tremula"
/mol_type="mRNA"
/db_xref="taxon:113636"
/clone="UB49DPG02"
/tissue_type="Active cambium"
/clone_lib="Populus active cambium cDNA library"

ORIGIN

Query Match 81.0%; Score 17; DB 14; Length 252;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGCAGCAGCGGTAATA 21
||||||||||||||||||
Db 189 CAGCAGCAGCGGTAATA 205

RESULT 9
AU007074/c
LOCUS AU007074 413 bp mRNA linear EST 31-JUL-1998
DEFINITION AU007074 Schizosaccharomyces pombe late log phase cDNA Schizosaccharomyces pombe cDNA clone spc01418, mRNA sequence.
ACCESSION AU007074
VERSION AU007074.1 GI:3343532
KEYWORDS EST.
SOURCE Schizosaccharomyces pombe (fission yeast)
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE 1 (bases 1 to 413)
AUTHORS Morimyo,M. and Mita,K.
TITLE Identification of expressed sequence tags of Schizosaccharomyces pombe
JOURNAL Unpublished (1998)
COMMENT Contact: Mitsuoki Morimyo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.

```
FEATURES             Location/Qualifiers
     source          1. .413
                     /organism="Schizosaccharomyces pombe"
                     /mol_type="mRNA"
                     /strain="972"
                     /db_xref="taxon:4896"
                     /clone="spc01418"
                     /sex="h minus"
                     /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
                     /note="Vector: M13mp19; The cDNA library of
                     Schizosaccharomyces pombe was prepared by cloning cDNA
                     into the SmaI site of M13mp19 DNA and the direction of DNA
                     sequences was not always from 5' to 3'. The cDNA data of
                     Schizosaccharomyces pombe are available for searching on
                     the World Wide Web.  (URL, http://www.nirs.go.jp)"
ORIGIN

  Query Match           81.0%;  Score 17;  DB 9;  Length 413;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGT 17
              |||||||||||||||||
Db         80 GTGCCAGCAGCAGCGGT 64


RESULT 10
BG632306/c
LOCUS       BG632306                460 bp    mRNA    linear   EST 23-APR-2001
DEFINITION  GH06375.3prime GH Drosophila melanogaster head pOT2 Drosophila
            melanogaster cDNA clone GH06375 3, mRNA sequence.
ACCESSION   BG632306
VERSION     BG632306.1  GI:13757423
KEYWORDS    EST.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 460)
  AUTHORS   Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
            Lewis,S. and Rubin,G.M.
  TITLE     BDGP/HHMI Drosophila EST Project
  JOURNAL   Unpublished (2001)
COMMENT     Other_ESTs: GH06375.5prime
            Contact: Stapleton, M.
            BDGP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            Based upon the presence of a XhoI site followed by a run of 14 or
            more T residues at the beginning of the sequence, this clone was
            polyadenylated. The resulting Poly-T sequence has been removed. hit
            genomic AE003763: arm:3R [23621985,23825541]
            estimated-cyto:98B1-98B6: 04/10/2001
            Plate: GH.63  row: G  column: 3
            High quality sequence stop: 444.
FEATURES             Location/Qualifiers
     source          1. .460
                     /organism="Drosophila melanogaster"
                     /mol_type="mRNA"
                     /db_xref="taxon:7227"
                     /clone="GH06375"
                     /sex="male and female"
                     /dev_stage="adult"
                     /lab_host="DH5 - alpha"
                     /clone_lib="GH Drosophila melanogaster head pOT2"
                     /note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
                     XhoI; Sized fractionated cDNAs were directly ligated into
                     pOT2.  Plasmid cDNA library."
ORIGIN

  Query Match           81.0%;  Score 17;  DB 12;  Length 460;
  Best Local Similarity   100.0%;  Pred. No. 5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGCCAGCAGCAGCGGTA 18
              |||||||||||||||||
Db        156 TGCCAGCAGCAGCGGTA 140


RESULT 11
AA695154/c
LOCUS       AA695154                475 bp    mRNA    linear   EST 23-APR-2001
DEFINITION  GM02326.3prime GM Drosophila melanogaster ovary BlueScript
            Drosophila melanogaster cDNA clone GM02326 3prime, mRNA sequence.
ACCESSION   AA695154
VERSION     AA695154.1  GI:2697774
KEYWORDS    EST.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 475)
  AUTHORS   Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
            Lewis,S. and Rubin,G.M.
  TITLE     BDGP/HHMI Drosophila EST Project
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Stapleton, M.
            BDGP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            Based upon the presence of a XhoI site followed by a run of 14 or
            more T residues at the beginning of the sequence, this clone
            probably contains an inverted insert. The sequence has been trimmed
            and the T residues removed.
            Plate: 23  row: C  column: 2
            High quality sequence stop: 406.
FEATURES             Location/Qualifiers
     source          1. .475
                     /organism="Drosophila melanogaster"
                     /mol_type="mRNA"
                     /db_xref="taxon:7227"
                     /clone="GM02326"
                     /sex="female"
                     /dev_stage="newly eclosed females: germarium-stage 6"
                     /lab_host="SOLR"
                     /clone_lib="GM Drosophila melanogaster ovary BlueScript"
                     /note="Organ: ovary; Vector: BlueScript SK; Site_1: EcoRI;
                     Site_2: XhoI; Constructed using Stratagene ZAP-cDNA
                     Synthesis kit. Oligo dT-primed and directionally cloned at
                     EcoRI and XhoI in BlueScript SK(+/-)"
ORIGIN

  Query Match           81.0%;  Score 17;  DB 9;  Length 475;
  Best Local Similarity   100.0%;  Pred. No. 5e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGCCAGCAGCAGCGGTA 18
              |||||||||||||||||
Db        156 TGCCAGCAGCAGCGGTA 140


RESULT 12
AW940266/c
LOCUS       AW940266                524 bp    mRNA    linear   EST 02-DEC-2003
DEFINITION  GH07623.3prime GH Drosophila melanogaster head pOT2 Drosophila
            melanogaster cDNA clone GH07623 3 similar to CG5514: FBan0005514
            GO:[] located on: 3R 98B2-98B2;: 08/12/2002, mRNA sequence.
ACCESSION   AW940266
VERSION     AW940266.1  GI:8115712
KEYWORDS    EST.
```

```
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 524)
  AUTHORS   Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
            Lewis,S. and Rubin,G.M.
  TITLE     BDGP/HHMI Drosophila EST Project
  JOURNAL   Unpublished (2001)
COMMENT     Other_ESTs: GH07623.5prime
            Contact: Stapleton, M.
            BDGP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            Based upon the presence of a XhoI site followed by a run of 14 or
            more T residues at the beginning of the sequence, this clone was
            polyadenylated. The resulting Poly-T sequence has been removed. hit
            genomic AE003763: Drosophila melanogaster genomic scaffold
            142000013386035 section 88 of 105, complete sequence.: 02/16/2001
            Plate: GH.76  row: B  column: 11
            High quality sequence stop: 382.
FEATURES             Location/Qualifiers
     source          1. .524
                     /organism="Drosophila melanogaster"
                     /mol_type="mRNA"
                     /db_xref="taxon:7227"
                     /clone="GH07623"
                     /sex="male and female"
                     /dev_stage="adult"
                     /lab_host="DH5 - alpha"
                     /clone_lib="GH Drosophila melanogaster head pOT2"
                     /note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
                     XhoI; Sized fractionated cDNAs were directly ligated into
                     pOT2.  Plasmid cDNA library."
ORIGIN

  Query Match             81.0%;  Score 17;  DB 10;  Length 524;
  Best Local Similarity   100.0%;  Pred. No. 5.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGCCAGCAGCAGCGGTA 18
              |||||||||||||||||
Db        156 TGCCAGCAGCAGCGGTA 140


RESULT 13
AI518472/c
LOCUS       AI518472                540 bp    mRNA    linear   EST 19-APR-2001
DEFINITION  LD37996.3prime LD Drosophila melanogaster embryo pOT2 Drosophila
            melanogaster cDNA clone LD37996 3prime, mRNA sequence.
ACCESSION   AI518472
VERSION     AI518472.1  GI:4424326
KEYWORDS    EST.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 540)
  AUTHORS   Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
            Lewis,S. and Rubin,G.M.
  TITLE     BDGP/HHMI Drosophila EST Project
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Stapleton, M.
            BDGP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            Based upon the presence of a XhoI site followed by a run of 14 or
            more T residues at the beginning of the sequence, this clone
            probably contains an inverted insert. The resulting Poly-T sequence
            has been removed.
            Plate: 379  row: H  column: 12
            High quality sequence stop: 440.
FEATURES             Location/Qualifiers
     source          1. .540
                     /organism="Drosophila melanogaster"
                     /mol_type="mRNA"
                     /db_xref="taxon:7227"
                     /clone="LD37996"
                     /sex="male and female"
                     /dev_stage="0 to 24 hours mixed stage embryonic"
                     /lab_host="XL1 Blue"
                     /clone_lib="LD Drosophila melanogaster embryo pOT2"
                     /note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2:
                     XhoI; Sized fractionated cDNAs were directly ligated into
                     pOT2. "
ORIGIN

  Query Match             81.0%;  Score 17;  DB 9;  Length 540;
  Best Local Similarity   100.0%;  Pred. No. 5.1e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGCCAGCAGCAGCGGTA 18
              |||||||||||||||||
Db        156 TGCCAGCAGCAGCGGTA 140


RESULT 14
BF331275/c
LOCUS       BF331275                554 bp    mRNA    linear   EST 22-NOV-2000
DEFINITION  RC5-BT0377-030200-012-G03 BT0377 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF331275
VERSION     BF331275.1  GI:11302023
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 554)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC5&t2=RC5-BT0377-
            030200-012-G03&t3=2000-02-03&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 74
            High quality sequence stop: 91.
FEATURES             Location/Qualifiers
     source          1. .554
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
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/clone_lib="BT0377"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
ORIGIN

Query Match 81.0%; Score 17; DB 10; Length 554;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCCAGCAGCAGCGGTAA 19
||||||||||||||||||
Db 49 GCCAGCAGCAGCGGTAA 33

RESULT 15
AI397756/c
LOCUS AI397756 619 bp mRNA linear EST 08-FEB-1999
DEFINITION NCC5H8T3 Conidial Neurospora crassa cDNA clone NC5H8 5', mRNA sequence.
ACCESSION AI397756
VERSION AI397756.1 GI:4240841
KEYWORDS EST.
SOURCE Neurospora crassa
ORGANISM Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
REFERENCE 1 (bases 1 to 619)
AUTHORS Nelson,M.A., Kang,S., Braun,E.L., Crawford,M.E., Dolan,P.L., Leonard,P.M., Mitchell,J., Armijo,A.M., Bean,L., Blueyes,E., Cushing,T., Errett,A., Fleharty,M., Gorman,M., Judson,K., Miller,R., Ortega,J., Pavlova,I., Perea,J., Todisco,S., Trujillo,R., Valentine,J., Wells,A., Werner-Washburne,M., Yazzie,S. and Natvig,D.O.
TITLE Expressed sequences from conidial, mycelial, and sexual stages of Neurospora crassa
JOURNAL Fungal Genet. Biol. 21, 348-363 (1997)
MEDLINE 97435549
PUBMED 9290248
COMMENT Contact: Natvig,D.O./Nelson,M.A.
Department of Biology
University of New Mexico
Castetter Hall, Albuquerque, NM 87131, USA
Tel: 505 277 3411
Fax: 505 277 0304
Email: ngp@biology.unm.edu.
FEATURES Location/Qualifiers
source 1. .619
/organism="Neurospora crassa"
/mol_type="mRNA"
/strain="74-OR23-IV A"
/db_xref="taxon:5141"
/clone="NC5H8"
/sex="Mating type A"
/tissue_type="Conidia"
/dev_stage="germinating conidia"
/clone_lib="Conidial"
/note="mRNA isolated from germinating conidia, grown in 1x Vogel's, 2% sucrose for 4.5 hours. cDNA directionally cloned into pBluescript SK(-) using the Uni-ZAP XR vector system (Stratagene, La Jolla, CA)."
ORIGIN

Query Match 81.0%; Score 17; DB 9; Length 619;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGGT 17
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Db 279 GTGCCAGCAGCAGCGGT 263

Search completed: August 4, 2004, 09:20:58
Job time : 1466.92 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 06:43:54 ; Search time 218.94 Seconds
(without alignments)
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Title: US-09-940-860-3
Perfect score: 22
Sequence: 1 acaaggcccgagaacgtattca 22

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4754066 seqs, 1232178907 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9508132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_New:*
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9: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	16	72.7	1502	7	US-10-729-961-4	Sequence 4, Appli
c	2	16	72.7	1661	7	US-10-729-961-1	Sequence 1, Appli
c	3	16	72.7	8004	5	US-09-404-520B-5583	Sequence 5583, Ap
c	4	15	68.2	281443	6	US-10-896-891-531	Sequence 531, App
	5	14	63.6	1071	7	US-10-100-683-3306	Sequence 3306, Ap
	6	14	63.6	1080	5	US-09-404-520B-27485	Sequence 27485, A
	7	14	63.6	1215	5	US-09-248-796A-3573	Sequence 3573, Ap
	8	14	63.6	1271	7	US-10-767-701-12478	Sequence 12478, A
	9	14	63.6	1379	5	US-09-404-520B-9481	Sequence 9481, Ap
	10	14	63.6	1389	5	US-09-404-520B-20466	Sequence 20466, A
	11	14	63.6	1553	6	US-10-425-115-166711	Sequence 166711,
	12	14	63.6	1866	5	US-09-404-520B-14910	Sequence 14910, A
c	13	14	63.6	1959	7	US-10-100-683-2841	Sequence 2841, Ap
c	14	14	63.6	2307	7	US-10-745-444-764	Sequence 764, App
	15	14	63.6	2783	6	US-10-501-933-4270	Sequence 4270, Ap
	16	14	63.6	2783	9	US-60-559-949-602	Sequence 602, App
c	17	14	63.6	10088	7	US-10-100-683-13121	Sequence 13121, A
c	18	14	63.6	67163	7	US-10-767-471-10712	Sequence 10712, A
c	19	14	63.6	77945	9	US-60-582-609-20052	Sequence 20052, A
	20	13	59.1	19	8	US-10-714-333A-495525	Sequence 495525,
	21	13	59.1	19	8	US-10-714-333A-600711	Sequence 600711,
	22	13	59.1	25	5	US-09-660-080C-10392	Sequence 10392, A
	23	13	59.1	25	7	US-10-843-527-118931	Sequence 118931,
c	24	13	59.1	25	7	US-10-843-527-119246	Sequence 119246,
c	25	13	59.1	49	5	US-09-404-520B-36908	Sequence 36908, A
c	26	13	59.1	60	9	US-60-579-902-11666	Sequence 11666, A
c	27	13	59.1	261	9	US-60-565-632-2213	Sequence 2213, Ap
c	28	13	59.1	261	9	US-60-579-062-2213	Sequence 2213, Ap
c	29	13	59.1	267	6	US-10-425-115-20380	Sequence 20380, A
c	30	13	59.1	327	7	US-10-834-967-2447	Sequence 2447, Ap
c	31	13	59.1	359	6	US-10-425-115-14666	Sequence 14666, A
	32	13	59.1	450	5	US-09-404-520B-8744	Sequence 8744, Ap
c	33	13	59.1	450	5	US-09-404-520B-20686	Sequence 20686, A
	34	13	59.1	471	5	US-09-404-520B-26196	Sequence 26196, A
	35	13	59.1	480	1	PCT-US04-17686-2675	Sequence 2675, Ap
	36	13	59.1	500	6	US-10-425-115-108619	Sequence 108619,
	37	13	59.1	516	7	US-10-767-701-28589	Sequence 28589, A
	38	13	59.1	601	6	US-10-896-891-9568	Sequence 9568, Ap
	39	13	59.1	601	6	US-10-896-891-9569	Sequence 9569, Ap
	40	13	59.1	658	1	PCT-US04-08371A-304	Sequence 304, App
	41	13	59.1	702	7	US-10-724-972A-2882	Sequence 2882, Ap
	42	13	59.1	749	6	US-10-425-115-97664	Sequence 97664, A
	43	13	59.1	750	6	US-10-425-115-164349	Sequence 164349,
	44	13	59.1	759	9	US-60-554-981-1436	Sequence 1436, Ap
	45	13	59.1	1146	7	US-10-100-683-1635	Sequence 1635, Ap

ALIGNMENTS

RESULT 1
US-10-729-961-4/c
; Sequence 4, Application US/10729961
; GENERAL INFORMATION:
; APPLICANT: IWASE, Tadayuki
; APPLICANT: ITANO, Morihide
; APPLICANT: YANO, Yoshitaka
; TITLE OF INVENTION: Primers For Detecting Fusobacterium Nucleatum By Pcr Methods And
; TITLE OF INVENTION: For Detection
; FILE REFERENCE: 246312US0
; CURRENT APPLICATION NUMBER: US/10/729,961
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: JP 2002-358698
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: JP 2003-403715
; PRIOR FILING DATE: 2003-12-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1502
; TYPE: DNA
; ORGANISM: Fusobacterium nucleatum
US-10-729-961-4

Query Match 72.7%; Score 16; DB 7; Length 1502;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          7 CCCGAGAACGTATTCA 22
              ||||||||||||||||
Db       1367 CCCGAGAACGTATTCA 1352
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RESULT 2
US-10-729-961-1/c
; Sequence 1, Application US/10729961
; GENERAL INFORMATION:
; APPLICANT: IWASE, Tadayuki
; APPLICANT: ITANO, Morihide
; APPLICANT: YANO, Yoshitaka
; TITLE OF INVENTION: Primers For Detecting Fusobacterium Nucleatum By Pcr Methods And
; TITLE OF INVENTION: For Detection
; FILE REFERENCE: 246312US0
; CURRENT APPLICATION NUMBER: US/10/729,961
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: JP 2002-358698
; PRIOR FILING DATE: 2002-12-10

; PRIOR APPLICATION NUMBER: JP 2003-403715
; PRIOR FILING DATE: 2003-12-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1661
; TYPE: DNA
; ORGANISM: Fusobacterium nucleatum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1650)..(1650)
; OTHER INFORMATION: n stands for any base
US-10-729-961-1

Query Match 72.7%; Score 16; DB 7; Length 1661;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCCGAGAACGTATTCA 22
||||||||||||||||
Db 1367 CCCGAGAACGTATTCA 1352

RESULT 3
US-09-404-520B-5583/c
; Sequence 5583, Application US/09404520B
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Timberlake, William E.
; APPLICANT: McIninch, James
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Ghodssi, Azita
; TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-10(15498)A
; CURRENT APPLICATION NUMBER: US/09/404,520B
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 44345
; SEQ ID NO 5583
; LENGTH: 8004
; TYPE: DNA
; ORGANISM: Emericella nidulans
US-09-404-520B-5583

Query Match 72.7%; Score 16; DB 5; Length 8004;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCCGAGAACGTATTCA 22
||||||||||||||||
Db 771 CCCGAGAACGTATTCA 756

RESULT 4
US-10-896-891-531/c
; Sequence 531, Application US/10896891
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH CANCER, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL000788
; CURRENT APPLICATION NUMBER: US/10/896,891
; CURRENT FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 60/231,328
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 12618
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 531
; LENGTH: 281443
; TYPE: DNA
; ORGANISM: Human
US-10-896-891-531

Query Match 68.2%; Score 15; DB 6; Length 281443;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GCCCGAGAACGTATT 20
|||||||||||||||
Db 240133 GCCCGAGAACGTATT 240119

RESULT 5
US-10-100-683-3306
; Sequence 3306, Application US/10100683
; GENERAL INFORMATION:
; APPLICANT: Rosen, et al.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS900
; CURRENT APPLICATION NUMBER: US/10/100,683
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: US 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,845
; PRIOR FILING DATE: 1997-08-22
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; PRIOR FILING DATE: 1997-04-11
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; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-08-22
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; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,632
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,892
; PRIOR FILING DATE: 1997-08-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13468
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3306
; LENGTH: 1071
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-100-683-3306

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Qy 2 CAAGGCCCGAGAAC 15
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Db 103 CAAGGCCCGAGAAC 116

RESULT 6
US-09-404-520B-27485
; Sequence 27485, Application US/09404520B
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Timberlake, William E.
; APPLICANT: McIninch, James
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Ghodssi, Azita
; TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-10(15498)A
; CURRENT APPLICATION NUMBER: US/09/404,520B
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 44345
; SEQ ID NO 27485
; LENGTH: 1080

; TYPE: DNA
; ORGANISM: Emericella nidulans
US-09-404-520B-27485

Query Match 63.6%; Score 14; DB 5; Length 1080;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CGAGAACGTATTCA 22
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Db 904 CGAGAACGTATTCA 917

RESULT 7
US-09-248-796A-3573
; Sequence 3573, Application US/09248796A
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 3573
; LENGTH: 1215
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-3573

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Best Local Similarity 100.0%; Pred. No. 10;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAAGGCCCGAGAA 14
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Db 1151 ACAAGGCCCGAGAA 1164

RESULT 8
US-10-767-701-12478
; Sequence 12478, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 12478
; LENGTH: 1271
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS1265_1
US-10-767-701-12478

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Best Local Similarity 100.0%; Pred. No. 10;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GCCCGAGAACGTAT 19
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Db 832 GCCCGAGAACGTAT 845

RESULT 9
US-09-404-520B-9481
; Sequence 9481, Application US/09404520B
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Timberlake, William E.
; APPLICANT: McIninch, James
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Ghodssi, Azita
; TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-10(15498)A
; CURRENT APPLICATION NUMBER: US/09/404,520B
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 44345
; SEQ ID NO 9481
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: Emericella nidulans
US-09-404-520B-9481

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Qy 9 CGAGAACGTATTCA 22
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Db 1096 CGAGAACGTATTCA 1109

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; Sequence 20466, Application US/09404520B
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Timberlake, William E.
; APPLICANT: McIninch, James
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Ghodssi, Azita
; TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-10(15498)A
; CURRENT APPLICATION NUMBER: US/09/404,520B
; CURRENT FILING DATE: 1999-09-23
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; TYPE: DNA
; ORGANISM: Emericella nidulans
US-09-404-520B-20466

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Best Local Similarity 100.0%; Pred. No. 10;
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Qy 4 AGGCCCGAGAACGT 17
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Db 365 AGGCCCGAGAACGT 378

RESULT 11
US-10-425-115-166711
; Sequence 166711, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 166711
; LENGTH: 1553
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_83619C.1
US-10-425-115-166711

Query Match 63.6%; Score 14; DB 6; Length 1553;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AGGCCCGAGAACGT 17
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Db 1207 AGGCCCGAGAACGT 1220

RESULT 12
US-09-404-520B-14910
; Sequence 14910, Application US/09404520B
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Timberlake, William E.
; APPLICANT: McIninch, James
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Ghodssi, Azita
; TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-10(15498)A
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; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 44345
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; LENGTH: 1866
; TYPE: DNA
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US-09-404-520B-14910

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 424 AGGCCCGAGAACGT 437

RESULT 13
US-10-100-683-2841/c
; Sequence 2841, Application US/10100683
; GENERAL INFORMATION:
; APPLICANT: Rosen, et al.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS900
; CURRENT APPLICATION NUMBER: US/10/100,683
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: US 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,599
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,632
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,892
; PRIOR FILING DATE: 1997-08-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13468
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2841
; LENGTH: 1959
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-100-683-2841

Query Match 63.6%; Score 14; DB 7; Length 1959;
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGCCCGAGAACGTA 18
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Db 1223 GGCCCGAGAACGTA 1210

RESULT 14
US-10-745-444-764/c
; Sequence 764, Application US/10745444
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DETECTING EXPRESSION OF GENES ENCODING SECRETED PROTEINS
; FILE REFERENCE: PA-0017 US
; CURRENT APPLICATION NUMBER: US/10/745,444
; CURRENT FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 809
; SOFTWARE: PERL Program
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; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1997168CT1
; PUBLICATION INFORMATION:
US-10-745-444-764

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Db 236 GGCCCGAGAACGTA 223

RESULT 15
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; Sequence 4270, Application US/10501933
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Hepatotoxicology Modeling
; FILE REFERENCE: 44921-5038-01-WO
; CURRENT APPLICATION NUMBER: US/10/501,933
; CURRENT FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880

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;  PRIOR FILING DATE: 2001-05-22
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;  PRIOR FILING DATE: 2001-06-19
;  PRIOR APPLICATION NUMBER: US 60/303,459
;  PRIOR FILING DATE: 2001-07-09
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;  PRIOR FILING DATE: 2001-11-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 4295
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4270
;   LENGTH: 2783
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;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. X83231
US-10-501-933-4270

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SUMMARIES

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1	22	100.0	22	39	US-09-940-860-3	Sequence 3, Appli
c 2	22	100.0	336	1	PCT-US01-16030A-2	Sequence 2, Appli
c 3	22	100.0	336	1	PCT-US03-03202-2	Sequence 2, Appli
c 4	22	100.0	336	1	PCT-US03-03202A-2	Sequence 2, Appli
c 5	22	100.0	336	35	US-09-860-200D-2	Sequence 2, Appli
c 6	22	100.0	368	3	US-07-923-871B-36	Sequence 36, Appl
c 7	22	100.0	370	3	US-07-923-871B-35	Sequence 35, Appl
c 8	22	100.0	498	3	US-07-923-871B-1	Sequence 1, Appli
c 9	22	100.0	505	3	US-07-923-871-1	Sequence 1, Appli
c 10	22	100.0	505	3	US-07-923-871A-1	Sequence 1, Appli
c 11	22	100.0	1014	44	US-10-061-071-94	Sequence 94, Appl
c 12	22	100.0	1377	23	US-09-548-998A-2	Sequence 2, Appli
c 13	22	100.0	1377	23	US-09-548-998A-4	Sequence 4, Appli
c 14	22	100.0	1377	23	US-09-548-998A-5	Sequence 5, Appli
c 15	22	100.0	1377	23	US-09-548-998A-6	Sequence 6, Appli
c 16	22	100.0	1377	23	US-09-548-998C-2	Sequence 2, Appli
c 17	22	100.0	1377	23	US-09-548-998C-4	Sequence 4, Appli
c 18	22	100.0	1377	23	US-09-548-998C-5	Sequence 5, Appli
c 19	22	100.0	1377	23	US-09-548-998C-6	Sequence 6, Appli
c 20	22	100.0	1377	23	US-09-548-998E-2	Sequence 2, Appli
c 21	22	100.0	1377	23	US-09-548-998E-4	Sequence 4, Appli
c 22	22	100.0	1377	23	US-09-548-998E-5	Sequence 5, Appli
c 23	22	100.0	1377	23	US-09-548-998E-6	Sequence 6, Appli
c 24	22	100.0	1377	44	US-10-061-071-2	Sequence 2, Appli
c 25	22	100.0	1377	44	US-10-061-071-4	Sequence 4, Appli
c 26	22	100.0	1377	44	US-10-061-071-5	Sequence 5, Appli
c 27	22	100.0	1377	44	US-10-061-071-6	Sequence 6, Appli
c 28	22	100.0	1378	23	US-09-548-998A-3	Sequence 3, Appli
c 29	22	100.0	1378	23	US-09-548-998C-3	Sequence 3, Appli
c 30	22	100.0	1378	23	US-09-548-998E-3	Sequence 3, Appli
c 31	22	100.0	1378	44	US-10-061-071-3	Sequence 3, Appli
c 32	22	100.0	1443	23	US-09-548-998A-7	Sequence 7, Appli
c 33	22	100.0	1443	23	US-09-548-998C-7	Sequence 7, Appli
c 34	22	100.0	1443	23	US-09-548-998E-7	Sequence 7, Appli
c 35	22	100.0	1443	44	US-10-061-071-7	Sequence 7, Appli
c 36	22	100.0	1451	32	US-09-786-253-4	Sequence 4, Appli
c 37	22	100.0	1451	32	US-09-786-253-5	Sequence 5, Appli
38	22	100.0	116217	1	PCT-US98-12764-2	Sequence 2, Appli
39	22	100.0	116217	34	US-09-830-228-2	Sequence 2, Appli
c 40	22	100.0	910715	1	PCT-US98-12764-1	Sequence 1, Appli
c 41	22	100.0	910715	34	US-09-830-228-1	Sequence 1, Appli
c 42	22	100.0	1230025	48	US-10-289-762-1	Sequence 1, Appli
c 43	22	100.0	1230230	20	US-09-438-185-1	Sequence 1, Appli
c 44	22	100.0	1230230	20	US-09-438-185A-1	Sequence 1, Appli
45	21	95.5	1555893	12	US-08-895-611-1	Sequence 1, Appli

ALIGNMENTS

```
RESULT 1
US-09-940-860-3
; Sequence 3, Application US/09940860
; GENERAL INFORMATION:
;  APPLICANT: Rothman, Richard
;  APPLICANT:  Majmudar, Maulik
;  TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
;  FILE REFERENCE: 01107.00185
;  CURRENT APPLICATION NUMBER: US/09/940,860
;  CURRENT FILING DATE:  2001-08-29
;  PRIOR APPLICATION NUMBER: 60/229,376
;  PRIOR FILING DATE: 2000-08-31
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic amplification primer
US-09-940-860-3

  Query Match           100.0%;  Score 22;  DB 39;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 0.0095;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db          1 ACAAGGCCCGAGAACGTATTCA 22


RESULT 2
PCT-US01-16030A-2/c
; Sequence 2, Application PC/TUS0116030A
; GENERAL INFORMATION:
;  APPLICANT: University of Maryland Biotechnology Institute
;  APPLICANT:  Sowers, Kevin R.
;  APPLICANT:  May, Harold D.
;  TITLE OF INVENTION: Compositions and Methods for Microbial Dechlorination of Polychlo
;  TITLE OF INVENTION:  Biphenyl Compounds
;  FILE REFERENCE: 4115-149 PCT
;  CURRENT APPLICATION NUMBER: PCT/US01/16030A
;  CURRENT FILING DATE:  2001-05-18
;  PRIOR APPLICATION NUMBER: US 60/205,818
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 60/266,650
;  PRIOR FILING DATE: 2001-02-06
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 336
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
PCT-US01-16030A-2

  Query Match           100.0%;  Score 22;  DB 1;  Length 336;
  Best Local Similarity  100.0%;  Pred. No. 0.0076;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        323 ACAAGGCCCGAGAACGTATTCA 302


RESULT 3
PCT-US03-03202-2/c
; Sequence 2, Application PC/TUS0303202
; GENERAL INFORMATION:
;  APPLICANT: University of Maryland Biotechnology Institute
;  TITLE OF INVENTION: Stimulation of Microbial Dechlorination of Polychlorinated Biphen
;  TITLE OF INVENTION:  Halogenated Ethenes
;  FILE REFERENCE: 4115-176 PCT
;  CURRENT APPLICATION NUMBER: PCT/US03/03202
;  CURRENT FILING DATE:  2003-02-03
;  PRIOR APPLICATION NUMBER: 60/353,134
;  PRIOR FILING DATE: 2002-02-01
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 336
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
PCT-US03-03202-2

  Query Match           100.0%;  Score 22;  DB 1;  Length 336;
  Best Local Similarity  100.0%;  Pred. No. 0.0076;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        323 ACAAGGCCCGAGAACGTATTCA 302


RESULT 4
PCT-US03-03202A-2/c
; Sequence 2, Application PC/TUS0303202A
; GENERAL INFORMATION:
;  APPLICANT: University of Maryland Biotechnology Institute
;  TITLE OF INVENTION: Stimulation of Microbial Dechlorination of Polychlorinated Biphen
;  TITLE OF INVENTION:  Halogenated Ethenes
;  FILE REFERENCE: 4115-176 PCT
;  CURRENT APPLICATION NUMBER: PCT/US03/03202A
;  CURRENT FILING DATE:  2003-02-03
;  PRIOR APPLICATION NUMBER: 60/353,134
;  PRIOR FILING DATE: 2002-02-01
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 336
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
PCT-US03-03202A-2

  Query Match             100.0%;  Score 22;  DB 1;  Length 336;
  Best Local Similarity   100.0%;  Pred. No. 0.0076;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        323 ACAAGGCCCGAGAACGTATTCA 302


RESULT 5
US-09-860-200D-2/c
; Sequence 2, Application US/09860200D
; GENERAL INFORMATION:
;  APPLICANT: Kevin, Bowers R.
;  APPLICANT:  Harold, May D.
;  TITLE OF INVENTION: Compositions and Methods for Microbial Dechlorination of
;  TITLE OF INVENTION:  Polychlorinated Biphenyl Compounds
;  FILE REFERENCE: 4115-149
;  CURRENT APPLICATION NUMBER: US/09/860,200D
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/205,818
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 60/266,650
;  PRIOR FILING DATE: 2001-02-06
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 336
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-09-860-200D-2

  Query Match             100.0%;  Score 22;  DB 35;  Length 336;
  Best Local Similarity   100.0%;  Pred. No. 0.0076;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        323 ACAAGGCCCGAGAACGTATTCA 302


RESULT 6
US-07-923-871B-36/c
; Sequence 36, Application US/07923871B
;  GENERAL INFORMATION:
;    APPLICANT:  White Ph.D, Thomas J.
;    APPLICANT:  Dodge, Deborah E.
;    TITLE OF INVENTION:  Method for Diagnosis of Lyme Disease
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/923,871B
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 489,676
;      FILING DATE:  07-MAR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petry, Douglas A.
;      REGISTRATION NUMBER:  35,321
;      REFERENCE/DOCKET NUMBER:  8697
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814-2974
;      TELEFAX:  (510) 814-2977
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  368 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-923-871B-36

  Query Match             100.0%;  Score 22;  DB 3;  Length 368;
  Best Local Similarity   100.0%;  Pred. No. 0.0076;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        273 ACAAGGCCCGAGAACGTATTCA 252


RESULT 7
US-07-923-871B-35/c
; Sequence 35, Application US/07923871B
;  GENERAL INFORMATION:
;    APPLICANT:  White Ph.D, Thomas J.
;    APPLICANT:  Dodge, Deborah E.
;    TITLE OF INVENTION:  Method for Diagnosis of Lyme Disease
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/923,871B
;      FILING DATE:
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;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 489,676
;      FILING DATE:  07-MAR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petry, Douglas A.
;      REGISTRATION NUMBER:  35,321
;      REFERENCE/DOCKET NUMBER:  8697
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814-2974
;      TELEFAX:  (510) 814-2977
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  370 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-923-871B-35

  Query Match             100.0%;  Score 22;  DB 3;  Length 370;
  Best Local Similarity   100.0%;  Pred. No. 0.0076;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        275 ACAAGGCCCGAGAACGTATTCA 254


RESULT 8
US-07-923-871B-1/c
; Sequence 1, Application US/07923871B
;  GENERAL INFORMATION:
;    APPLICANT:  White Ph.D, Thomas J.
;    APPLICANT:  Dodge, Deborah E.
;    TITLE OF INVENTION:  Method for Diagnosis of Lyme Disease
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/923,871B
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 489,676
;      FILING DATE:  07-MAR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petry, Douglas A.
;      REGISTRATION NUMBER:  35,321
;      REFERENCE/DOCKET NUMBER:  8697
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814-2974
;      TELEFAX:  (510) 814-2977
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  498 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (35..36)
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (41)
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (67)
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (164..165)
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (167)
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (169)
US-07-923-871B-1

  Query Match             100.0%;  Score 22;  DB 3;  Length 498;
  Best Local Similarity   100.0%;  Pred. No. 0.0074;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        396 ACAAGGCCCGAGAACGTATTCA 375


RESULT 9
US-07-923-871-1/c
; Sequence 1, Application US/07923871
;  GENERAL INFORMATION:
;    APPLICANT:  White Ph.D, Thomas J.
;    APPLICANT:  Dodge, Deborah E.
;    TITLE OF INVENTION:  Method for Diagnosis of Lyme Disease
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/923,871
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 489,676
;      FILING DATE:  07-MAR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sias, Stacey R.
;      REGISTRATION NUMBER:  32,630
;      REFERENCE/DOCKET NUMBER:  8697
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814-2863
;      TELEFAX:  (510) 522-1285
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  505 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
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;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (35..36)
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (41)
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (67)
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (164..165)
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (167)
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (169)
US-07-923-871-1

  Query Match           100.0%;  Score 22;  DB 3;  Length 505;
  Best Local Similarity  100.0%;  Pred. No. 0.0074;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        396 ACAAGGCCCGAGAACGTATTCA 375


RESULT 10
US-07-923-871A-1/c
; Sequence 1, Application US/07923871A
;  GENERAL INFORMATION:
;    APPLICANT:  White Ph.D, Thomas J.
;    APPLICANT:  Dodge, Deborah E.
;    TITLE OF INVENTION:  Method for Diagnosis of Lyme Disease
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/923,871A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 489,676
;      FILING DATE:  07-MAR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sias, Stacey R.
;      REGISTRATION NUMBER:  32,630
;      REFERENCE/DOCKET NUMBER:  8697
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 814-2863
;      TELEFAX:  (510) 522-1285
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  505 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (35..36)
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (41)
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (67)
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (164..165)
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (167)
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  complement (169)
US-07-923-871A-1

  Query Match           100.0%;  Score 22;  DB 3;  Length 505;
  Best Local Similarity  100.0%;  Pred. No. 0.0074;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        396 ACAAGGCCCGAGAACGTATTCA 375


RESULT 11
US-10-061-071-94/c
; Sequence 94, Application US/10061071
; GENERAL INFORMATION:
;  APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
;  APPLICANT:  HENDRICKSON,  EDWIN
;  TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
;  TITLE OF INVENTION:  BACTERIA
;  FILE REFERENCE: BC1002 US CIP
;  CURRENT APPLICATION NUMBER: US/10/061,071
;  CURRENT FILING DATE:  2002-01-29
;  PRIOR APPLICATION NUMBER: US 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  PRIOR APPLICATION NUMBER: 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  NUMBER OF SEQ ID NOS: 103
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 94
;   LENGTH: 1014
;   TYPE: DNA
;   ORGANISM: Dehalococcoides related Family A Group
US-10-061-071-94

  Query Match           100.0%;  Score 22;  DB 44;  Length 1014;
  Best Local Similarity  100.0%;  Pred. No. 0.007;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db       1004 ACAAGGCCCGAGAACGTATTCA 983


RESULT 12
US-09-548-998A-2/c
; Sequence 2, Application US/09548998A
; GENERAL INFORMATION:
;  APPLICANT: Ebersole, Richard C.
;  APPLICANT:  Hendrickson, Edwin
;  TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
;  TITLE OF INVENTION:  BACTERIA
;  FILE REFERENCE: BC1002 US NA
;  CURRENT APPLICATION NUMBER: US/09/548,998A
;  CURRENT FILING DATE:  2001-09-10
```

```
;  PRIOR APPLICATION NUMBER: 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
;    LENGTH: 1377
;    TYPE: DNA
;    ORGANISM: Dehalococcoides ethenogenes
US-09-548-998A-2

  Query Match           100.0%;  Score 22;  DB 23;  Length 1377;
  Best Local Similarity  100.0%;  Pred. No. 0.0068;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db       1321 ACAAGGCCCGAGAACGTATTCA 1300


RESULT 13
US-09-548-998A-4/c
; Sequence 4, Application US/09548998A
; GENERAL INFORMATION:
;  APPLICANT: Ebersole, Richard C.
;  APPLICANT:  Hendrickson, Edwin
;  TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
;  TITLE OF INVENTION:  BACTERIA
;  FILE REFERENCE: BC1002 US NA
;  CURRENT APPLICATION NUMBER: US/09/548,998A
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
;    LENGTH: 1377
;    TYPE: DNA
;    ORGANISM: Dehalococcoides ethenogenes
US-09-548-998A-4

  Query Match           100.0%;  Score 22;  DB 23;  Length 1377;
  Best Local Similarity  100.0%;  Pred. No. 0.0068;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db       1321 ACAAGGCCCGAGAACGTATTCA 1300


RESULT 14
US-09-548-998A-5/c
; Sequence 5, Application US/09548998A
; GENERAL INFORMATION:
;  APPLICANT: Ebersole, Richard C.
;  APPLICANT:  Hendrickson, Edwin
;  TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
;  TITLE OF INVENTION:  BACTERIA
;  FILE REFERENCE: BC1002 US NA
;  CURRENT APPLICATION NUMBER: US/09/548,998A
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
;    LENGTH: 1377
;    TYPE: DNA
;    ORGANISM: Dehalococcoides ethenogenes
US-09-548-998A-5

  Query Match           100.0%;  Score 22;  DB 23;  Length 1377;
  Best Local Similarity  100.0%;  Pred. No. 0.0068;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db       1321 ACAAGGCCCGAGAACGTATTCA 1300


RESULT 15
US-09-548-998A-6/c
; Sequence 6, Application US/09548998A
; GENERAL INFORMATION:
;  APPLICANT: Ebersole, Richard C.
;  APPLICANT:  Hendrickson, Edwin
;  TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
;  TITLE OF INVENTION:  BACTERIA
;  FILE REFERENCE: BC1002 US NA
;  CURRENT APPLICATION NUMBER: US/09/548,998A
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
;    LENGTH: 1377
;    TYPE: DNA
;    ORGANISM: Dehalococcoides ethenogenes
US-09-548-998A-6

  Query Match           100.0%;  Score 22;  DB 23;  Length 1377;
  Best Local Similarity  100.0%;  Pred. No. 0.0068;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db       1321 ACAAGGCCCGAGAACGTATTCA 1300


Search completed: August  4, 2004, 11:29:58
Job time : 2012.36 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 07:44:29 ; Search time 199.06 Seconds
(without alignments)
541.892 Million cell updates/sec

Title: US-09-940-860-3
Perfect score: 22
Sequence: 1 acaaggcccgagaacgtattca 22

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3222919 seqs, 2451570024 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	22	100.0	22	11	US-09-940-860-3	Sequence 3, Appli
c 2	22	100.0	336	10	US-09-860-200D-2	Sequence 2, Appli
c 3	22	100.0	1014	15	US-10-061-071-94	Sequence 94, Appl
c 4	22	100.0	1377	15	US-10-061-071-2	Sequence 2, Appli
c 5	22	100.0	1377	15	US-10-061-071-4	Sequence 4, Appli
c 6	22	100.0	1377	15	US-10-061-071-5	Sequence 5, Appli
c 7	22	100.0	1377	15	US-10-061-071-6	Sequence 6, Appli
c 8	22	100.0	1378	15	US-10-061-071-3	Sequence 3, Appli
c 9	22	100.0	1443	15	US-10-061-071-7	Sequence 7, Appli
c 10	22	100.0	1230025	16	US-10-289-762-1	Sequence 1, Appli
c 11	16	72.7	244	17	US-10-391-249-16	Sequence 16, Appl
c 12	16	72.7	354	17	US-10-391-249-17	Sequence 17, Appl
c 13	16	72.7	354	17	US-10-391-249-18	Sequence 18, Appl
c 14	16	72.7	683	14	US-10-053-078-1	Sequence 1, Appli
c 15	16	72.7	683	14	US-10-053-078-2	Sequence 2, Appli
c 16	16	72.7	1385	15	US-10-061-071-95	Sequence 95, Appl
c 17	16	72.7	105184	10	US-09-847-513A-1	Sequence 1, Appli
c 18	16	72.7	580073	15	US-10-205-220-1	Sequence 1, Appli
c 19	15	68.2	238484	13	US-10-087-192-544	Sequence 544, App
20	14	63.6	376	14	US-10-040-739-677	Sequence 677, App
21	14	63.6	417	16	US-10-393-840-230	Sequence 230, App
22	14	63.6	450	16	US-10-393-840-229	Sequence 229, App
23	14	63.6	457	10	US-09-918-995-32220	Sequence 32220, A
24	14	63.6	460	10	US-09-918-995-26732	Sequence 26732, A
25	14	63.6	472	15	US-10-066-543-2999	Sequence 2999, Ap
26	14	63.6	506	16	US-10-393-840-227	Sequence 227, App
27	14	63.6	511	10	US-09-918-995-38009	Sequence 38009, A
28	14	63.6	942	13	US-09-942-025-8	Sequence 8, Appli
c 29	14	63.6	1032	9	US-09-974-300-2328	Sequence 2328, Ap
30	14	63.6	1071	10	US-09-933-767-118	Sequence 118, App
31	14	63.6	1071	13	US-10-004-860-118	Sequence 118, App
32	14	63.6	1071	15	US-10-023-282-118	Sequence 118, App
33	14	63.6	1443	13	US-10-425-114-30504	Sequence 30504, A
34	14	63.6	1602	16	US-10-369-493-40891	Sequence 40891, A
35	14	63.6	5469	9	US-09-764-877-4000	Sequence 4000, Ap
36	14	63.6	5469	10	US-09-764-891-9371	Sequence 9371, Ap
37	14	63.6	5469	15	US-10-205-428-817	Sequence 817, App
38	14	63.6	5469	16	US-10-242-515-4000	Sequence 4000, Ap
39	14	63.6	9453	9	US-09-764-877-3999	Sequence 3999, Ap
40	14	63.6	9453	10	US-09-764-891-9370	Sequence 9370, Ap
41	14	63.6	9453	15	US-10-205-428-816	Sequence 816, App
42	14	63.6	9453	16	US-10-242-515-3999	Sequence 3999, Ap
c 43	14	63.6	35178	15	US-10-017-161-739	Sequence 739, App
44	14	63.6	46675	13	US-10-087-192-1255	Sequence 1255, Ap
c 45	14	63.6	67311	13	US-09-942-025-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-940-860-3
; Sequence 3, Application US/09940860
; Publication No. US20040005555A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, Richard
; APPLICANT: Majmudar, Maulik
; TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
; FILE REFERENCE: 01107.00185
; CURRENT APPLICATION NUMBER: US/09/940,860
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/229,376
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic amplification primer
US-09-940-860-3

Query Match 100.0%; Score 22; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db          1 ACAAGGCCCGAGAACGTATTCA 22
```

RESULT 2
US-09-860-200D-2/c
; Sequence 2, Application US/09860200D
; Publication No. US20030134408A1
; GENERAL INFORMATION:

```
;  APPLICANT: Kevin, Bowers R.
;  APPLICANT:  Harold, May D.
;  TITLE OF INVENTION: Compositions and Methods for Microbial Dechlorination of
;  TITLE OF INVENTION:  Polychlorinated Biphenyl Compounds
;  FILE REFERENCE: 4115-149
;  CURRENT APPLICATION NUMBER: US/09/860,200D
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/205,818
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 60/266,650
;  PRIOR FILING DATE: 2001-02-06
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 336
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-09-860-200D-2

  Query Match            100.0%;  Score 22;  DB 10;  Length 336;
  Best Local Similarity  100.0%;  Pred. No. 0.00047;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        323 ACAAGGCCCGAGAACGTATTCA 302


RESULT 3
US-10-061-071-94/c
; Sequence 94, Application US/10061071
; Publication No. US20030077601A1
; GENERAL INFORMATION:
;  APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
;  APPLICANT:  HENDRICKSON,  EDWIN
;  TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
;  TITLE OF INVENTION:  BACTERIA
;  FILE REFERENCE: BC1002 US CIP
;  CURRENT APPLICATION NUMBER: US/10/061,071
;  CURRENT FILING DATE:  2002-01-29
;  PRIOR APPLICATION NUMBER: US 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  PRIOR APPLICATION NUMBER: 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  NUMBER OF SEQ ID NOS: 103
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 94
;   LENGTH: 1014
;   TYPE: DNA
;   ORGANISM: Dehalococcoides related Family A Group
US-10-061-071-94

  Query Match            100.0%;  Score 22;  DB 15;  Length 1014;
  Best Local Similarity  100.0%;  Pred. No. 0.00045;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db       1004 ACAAGGCCCGAGAACGTATTCA 983


RESULT 4
US-10-061-071-2/c
; Sequence 2, Application US/10061071
; Publication No. US20030077601A1
; GENERAL INFORMATION:
;  APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
;  APPLICANT:  HENDRICKSON,  EDWIN
;  TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
;  TITLE OF INVENTION:  BACTERIA
;  FILE REFERENCE: BC1002 US CIP
;  CURRENT APPLICATION NUMBER: US/10/061,071
;  CURRENT FILING DATE:  2002-01-29
;  PRIOR APPLICATION NUMBER: US 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  PRIOR APPLICATION NUMBER: 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  NUMBER OF SEQ ID NOS: 103
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
;   LENGTH: 1377
;   TYPE: DNA
;   ORGANISM: Dehalococcoides ethenogenes strain PL
US-10-061-071-2

  Query Match            100.0%;  Score 22;  DB 15;  Length 1377;
  Best Local Similarity  100.0%;  Pred. No. 0.00045;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db       1321 ACAAGGCCCGAGAACGTATTCA 1300


RESULT 5
US-10-061-071-4/c
; Sequence 4, Application US/10061071
; Publication No. US20030077601A1
; GENERAL INFORMATION:
;  APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
;  APPLICANT:  HENDRICKSON,  EDWIN
;  TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
;  TITLE OF INVENTION:  BACTERIA
;  FILE REFERENCE: BC1002 US CIP
;  CURRENT APPLICATION NUMBER: US/10/061,071
;  CURRENT FILING DATE:  2002-01-29
;  PRIOR APPLICATION NUMBER: US 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  PRIOR APPLICATION NUMBER: 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  NUMBER OF SEQ ID NOS: 103
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
;   LENGTH: 1377
;   TYPE: DNA
;   ORGANISM: Dehalococcoides ethenogenes strain DAB
US-10-061-071-4

  Query Match            100.0%;  Score 22;  DB 15;  Length 1377;
  Best Local Similarity  100.0%;  Pred. No. 0.00045;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db       1321 ACAAGGCCCGAGAACGTATTCA 1300


RESULT 6
US-10-061-071-5/c
; Sequence 5, Application US/10061071
; Publication No. US20030077601A1
; GENERAL INFORMATION:
;  APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
;  APPLICANT:  HENDRICKSON,  EDWIN
;  TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
;  TITLE OF INVENTION:  BACTERIA
;  FILE REFERENCE: BC1002 US CIP
;  CURRENT APPLICATION NUMBER: US/10/061,071
;  CURRENT FILING DATE:  2002-01-29
;  PRIOR APPLICATION NUMBER: US 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  PRIOR APPLICATION NUMBER: 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  NUMBER OF SEQ ID NOS: 103
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;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
;   LENGTH: 1377
;   TYPE: DNA
;   ORGANISM: Dehalococcoides ethenogenes strain PIN
US-10-061-071-5

  Query Match             100.0%;  Score 22;  DB 15;  Length 1377;
  Best Local Similarity   100.0%;  Pred. No. 0.00045;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db       1321 ACAAGGCCCGAGAACGTATTCA 1300


RESULT 7
US-10-061-071-6/c
; Sequence 6, Application US/10061071
; Publication No. US20030077601A1
; GENERAL INFORMATION:
;  APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
;  APPLICANT:  HENDRICKSON,  EDWIN
;  TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
;  TITLE OF INVENTION:  BACTERIA
;  FILE REFERENCE: BC1002 US CIP
;  CURRENT APPLICATION NUMBER: US/10/061,071
;  CURRENT FILING DATE:  2002-01-29
;  PRIOR APPLICATION NUMBER: US 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  PRIOR APPLICATION NUMBER: 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  NUMBER OF SEQ ID NOS: 103
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
;   LENGTH: 1377
;   TYPE: DNA
;   ORGANISM: Dehalococcoides ethenogenes strain DLL
US-10-061-071-6

  Query Match             100.0%;  Score 22;  DB 15;  Length 1377;
  Best Local Similarity   100.0%;  Pred. No. 0.00045;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db       1321 ACAAGGCCCGAGAACGTATTCA 1300


RESULT 8
US-10-061-071-3/c
; Sequence 3, Application US/10061071
; Publication No. US20030077601A1
; GENERAL INFORMATION:
;  APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
;  APPLICANT:  HENDRICKSON,  EDWIN
;  TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
;  TITLE OF INVENTION:  BACTERIA
;  FILE REFERENCE: BC1002 US CIP
;  CURRENT APPLICATION NUMBER: US/10/061,071
;  CURRENT FILING DATE:  2002-01-29
;  PRIOR APPLICATION NUMBER: US 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  PRIOR APPLICATION NUMBER: 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  NUMBER OF SEQ ID NOS: 103
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
;   LENGTH: 1378
;   TYPE: DNA
;   ORGANISM: Dehalococcoides ethenogenes strain V/SFD
US-10-061-071-3

  Query Match             100.0%;  Score 22;  DB 15;  Length 1378;
  Best Local Similarity   100.0%;  Pred. No. 0.00045;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db       1322 ACAAGGCCCGAGAACGTATTCA 1301


RESULT 9
US-10-061-071-7/c
; Sequence 7, Application US/10061071
; Publication No. US20030077601A1
; GENERAL INFORMATION:
;  APPLICANT: E.I. DUPONT DE NEMOURS & COMPANY
;  APPLICANT:  HENDRICKSON,  EDWIN
;  TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING
;  TITLE OF INVENTION:  BACTERIA
;  FILE REFERENCE: BC1002 US CIP
;  CURRENT APPLICATION NUMBER: US/10/061,071
;  CURRENT FILING DATE:  2002-01-29
;  PRIOR APPLICATION NUMBER: US 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  PRIOR APPLICATION NUMBER: 60/129,511
;  PRIOR FILING DATE: 1999-04-15
;  NUMBER OF SEQ ID NOS: 103
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
;   LENGTH: 1443
;   TYPE: DNA
;   ORGANISM: Dehalococcoides ethenogenes strain 195
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1353)..(1353)
;   OTHER INFORMATION: N= unknown
US-10-061-071-7

  Query Match             100.0%;  Score 22;  DB 15;  Length 1443;
  Best Local Similarity   100.0%;  Pred. No. 0.00045;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db       1329 ACAAGGCCCGAGAACGTATTCA 1308


RESULT 10
US-10-289-762-1/c
; Sequence 1, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, prev
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
;   LENGTH: 1230025
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15000)
;   OTHER INFORMATION: n=a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (15001)..(30000)
;   OTHER INFORMATION: n=a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
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; LOCATION: (30001)..(45000)
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  Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAAGGCCCGAGAACGTATTCA 22
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Db 1012085 ACAAGGCCCGAGAACGTATTCA 1012064

RESULT 11
US-10-391-249-16/c
; Sequence 16, Application US/10391249
; Publication No. US20040091935A1
; GENERAL INFORMATION:
; APPLICANT: Doxsey, Stephen J.
; TITLE OF INVENTION: NEW STRAINS OF MYCOPLASMA HYORHINIS AS
; TITLE OF INVENTION: CAUSATIVE AGENT FOR SYSTEMIC SCLEROSIS
; FILE REFERENCE: 07917-142001
; CURRENT APPLICATION NUMBER: US/10/391,249
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US 60/364,801
; PRIOR FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-391-249-16

  Query Match 72.7%; Score 16; DB 17; Length 244;
  Best Local Similarity 100.0%; Pred. No. 2.8;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCCGAGAACGTATTCA 22
    ||||||||||||||||
Db 201 CCCGAGAACGTATTCA 186

RESULT 12
US-10-391-249-17/c
; Sequence 17, Application US/10391249
; Publication No. US20040091935A1
; GENERAL INFORMATION:
; APPLICANT: Doxsey, Stephen J.
; TITLE OF INVENTION: NEW STRAINS OF MYCOPLASMA HYORHINIS AS
; TITLE OF INVENTION: CAUSATIVE AGENT FOR SYSTEMIC SCLEROSIS
; FILE REFERENCE: 07917-142001
; CURRENT APPLICATION NUMBER: US/10/391,249
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US 60/364,801
; PRIOR FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-391-249-17

  Query Match 72.7%; Score 16; DB 17; Length 354;
  Best Local Similarity 100.0%; Pred. No. 2.8;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCCGAGAACGTATTCA 22
    ||||||||||||||||
Db 299 CCCGAGAACGTATTCA 284

RESULT 13
US-10-391-249-18/c
; Sequence 18, Application US/10391249
; Publication No. US20040091935A1
; GENERAL INFORMATION:
; APPLICANT: Doxsey, Stephen J.
; TITLE OF INVENTION: NEW STRAINS OF MYCOPLASMA HYORHINIS AS
; TITLE OF INVENTION: CAUSATIVE AGENT FOR SYSTEMIC SCLEROSIS
; FILE REFERENCE: 07917-142001
; CURRENT APPLICATION NUMBER: US/10/391,249
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US 60/364,801
; PRIOR FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Sus scrofa
US-10-391-249-18

  Query Match 72.7%; Score 16; DB 17; Length 354;
  Best Local Similarity 100.0%; Pred. No. 2.8;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCCGAGAACGTATTCA 22
    ||||||||||||||||
Db 299 CCCGAGAACGTATTCA 284

RESULT 14
US-10-053-078-1/c
; Sequence 1, Application US/10053078
; Publication No. US20020192672A1
; GENERAL INFORMATION:
; APPLICANT: Dawson, Jacqueline E.
; APPLICANT: Anderson, Burt
; TITLE OF INVENTION: Identification of a New Ehrlichia
; TITLE OF INVENTION: Species from a Patient Suffering From Ehrlichiosis
; FILE REFERENCE: 6395-62149
; CURRENT APPLICATION NUMBER: US/10/053,078
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: U.S. 09/061770
; PRIOR FILING DATE: 1998-04-16
; PRIOR APPLICATION NUMBER: U.S. 07/687,526
; PRIOR FILING DATE: 1991-04-18
; PRIOR APPLICATION NUMBER: U.S. 08/147,891

; PRIOR FILING DATE: 1993-11-05
; PRIOR APPLICATION NUMBER: U.S. 08/394,464
; PRIOR FILING DATE: 1995-02-27
; PRIOR APPLICATION NUMBER: U.S. 08/943,464
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Ehrlichia chaffeensis
US-10-053-078-1

Query Match 72.7%; Score 16; DB 14; Length 683;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          7 CCCGAGAACGTATTCA 22
              ||||||||||||||||
Db        579 CCCGAGAACGTATTCA 564
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RESULT 15
US-10-053-078-2/c
; Sequence 2, Application US/10053078
; Publication No. US20020192672A1
; GENERAL INFORMATION:
; APPLICANT: Dawson, Jacqueline E.
; APPLICANT: Anderson, Burt
; TITLE OF INVENTION: Identification of a New Ehrlichia
; TITLE OF INVENTION: Species from a Patient Suffering From Ehrlichiosis
; FILE REFERENCE: 6395-62149
; CURRENT APPLICATION NUMBER: US/10/053,078
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: U.S. 09/061770
; PRIOR FILING DATE: 1998-04-16
; PRIOR APPLICATION NUMBER: U.S. 07/687,526
; PRIOR FILING DATE: 1991-04-18
; PRIOR APPLICATION NUMBER: U.S. 08/147,891
; PRIOR FILING DATE: 1993-11-05
; PRIOR APPLICATION NUMBER: U.S. 08/394,464
; PRIOR FILING DATE: 1995-02-27
; PRIOR APPLICATION NUMBER: U.S. 08/943,464
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 683
; TYPE: DNA
; ORGANISM: E. Canis
US-10-053-078-2

Query Match 72.7%; Score 16; DB 14; Length 683;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          7 CCCGAGAACGTATTCA 22
              ||||||||||||||||
Db        579 CCCGAGAACGTATTCA 564
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Job time : 201.06 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 04:00:30 ; Search time 180.771 Seconds
(without alignments)
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Title: US-09-940-860-3
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Scoring table: OLIGO_NUC
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Searched: 3373863 seqs, 2124099041 residues

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	22	100.0	336	6	AAD37948	Aad37948 16S ribos
c	2	22	100.0	336	9	AAD58507	Aad58507 16S ribos
c	3	22	100.0	1014	8	AAD58049	Aad58049 Dehalococ
c	4	22	100.0	1284	4	AAH28398	Aah28398 Intergeni
c	5	22	100.0	1284	4	AAH28396	Aah28396 Intergeni
c	6	22	100.0	1284	4	AAH28401	Aah28401 Intergeni
c	7	22	100.0	1284	4	AAH28397	Aah28397 Intergeni
c	8	22	100.0	1284	4	AAH28399	Aah28399 Intergeni
c	9	22	100.0	1335	4	AAC62240	Aac62240 A 16S rDN
c	10	22	100.0	1377	8	AAD57959	Aad57959 Dehalococ
c	11	22	100.0	1377	8	AAD57957	Aad57957 Dehalococ
c	12	22	100.0	1377	8	AAD57961	Aad57961 Dehalococ
c	13	22	100.0	1377	8	AAD57960	Aad57960 Dehalococ
c	14	22	100.0	1378	8	AAD57958	Aad57958 Dehalococ
c	15	22	100.0	1443	4	AAC62244	Aac62244 A 16S rDN
c	16	22	100.0	1443	8	AAD57962	Aad57962 Dehalococ
c	17	22	100.0	1451	4	AAF31090	Aaf31090 Bacterial
c	18	22	100.0	1451	4	AAF31089	Aaf31089 Bacterial
c	19	22	100.0	1479	6	ABS71617	Abs71617 Rickettsi
c	20	22	100.0	1515	6	ABS71618	Abs71618 Borrelia
c	21	22	100.0	110000	2	AAX20248_04	Continuation (5 of
c	22	22	100.0	110000	2	AAX91990_10	Continuation (11 o
	23	22	100.0	116277	2	AAX20249	Aax20249 Borrelia
c	24	16	72.7	180	2	AAQ36494	Aaq36494 Mycoplasm
c	25	16	72.7	187	2	AAQ36491	Aaq36491 Mycoplasm
c	26	16	72.7	188	2	AAQ36493	Aaq36493 Mycoplasm
c	27	16	72.7	189	2	AAQ36490	Aaq36490 Mycoplasm
c	28	16	72.7	191	2	AAQ36495	Aaq36495 Mycoplasm
c	29	16	72.7	400	2	AAQ21032	Aaq21032 Region sp
c	30	16	72.7	444	2	AAQ21035	Aaq21035 Region sp
c	31	16	72.7	539	2	AAQ21034	Aaq21034 Region sp
c	32	16	72.7	683	2	AAQ15188	Aaq15188 Ehrlichia
c	33	16	72.7	683	2	AAV43697	Aav43697 Ehrlichia
c	34	16	72.7	683	8	ADA18591	Ada18591 E. canis
c	35	16	72.7	683	8	ADA18587	Ada18587 E. chaffe
c	36	16	72.7	683	8	ACD26696	Acd26696 Ehrlichia
c	37	16	72.7	683	8	ACD26697	Acd26697 Ehrlichia
c	38	16	72.7	683	8	ABX93090	Abx93090 DNA seque
c	39	16	72.7	683	8	ABX93091	Abx93091 DNA seque
c	40	16	72.7	938	2	AAX61135	Aax61135 P36 ribos
c	41	16	72.7	938	2	AAX61134	Aax61134 P36 ribos
c	42	16	72.7	1385	8	AAD58050	Aad58050 Dehalococ
c	43	16	72.7	1438	7	ABZ79794	Abz79794 Mycoplasm
c	44	16	72.7	1445	7	ABZ79792	Abz79792 Mycoplasm
c	45	16	72.7	1445	7	ABZ79793	Abz79793 Mycoplasm

ALIGNMENTS

RESULT 1
AAD37948/c
ID AAD37948 standard; DNA; 336 BP.
XX
AC AAD37948;
XX
DT 10-SEP-2002 (first entry)
XX
DE 16S ribosomal DNA (rDNA) #2.
XX
KW Bioremediative microorganism; 16S ribosomal subunit; dechlorination; PCB;
KW polychlorinated biphenyl; biodegradation; halogenated organic waste;
KW contaminated soil; leachate; aqueous surfactant solution; ds.
XX
OS Unidentified.
XX
PN WO200189729-A2.
XX
PD 29-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-US016030.
XX
PR 19-MAY-2000; 2000US-0205818P.
PR 06-FEB-2001; 2001US-0266650P.
XX
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX
PI Sowers KR, May HD;
XX
DR WPI; 2002-114266/15.
XX
PT Bioremediative microorganism for dechlorinating chlorinated biphenyls and
PT for bioremediation, comprises a specific 16S ribosomal subunit nucleic
PT acid sequence.
XX
PS Claim 1; Fig 22; 102pp; English.
XX
CC The present invention relates to bioremediative microorganisms comprising
CC 16S ribosomal subunit nucleic acid sequence. The microorganisms of the
CC invention are useful for dechlorinating polychlorinated biphenyls (PCBs)
CC including anaerobic dechlorination of ortho- and double-flanked chloro
CC substituents of PCBs. They are useful for biodegradation of halogenated
CC organic waste, e.g., contaminated soil from landfill sites and river beds
CC containing PCBs and to treat leachates and aqueous surfactant solutions
CC resulting from washing the organic waste to transfer PCBs to the aqueous
CC surfactant solutions. The method of the invention is useful for

```
CC   determining the bioremediative potential of CB-containing site, which is
CC   useful for monitoring CB-containing site. The invention also relates to
CC   compositions which are useful for bioremediation. The present sequence is
CC   a 16S ribosomal DNA (rDNA) of the invention
XX
SQ   Sequence 336 BP; 76 A; 83 C; 97 G; 80 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 6;  Length 336;
  Best Local Similarity   100.0%;  Pred. No. 0.00072;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        323 ACAAGGCCCGAGAACGTATTCA 302


RESULT 2
AAD58507/c
ID   AAD58507 standard; DNA; 336 BP.
XX
AC   AAD58507;
XX
DT   04-DEC-2003  (first entry)
XX
DE   16S ribosomal subunit DNA #2.
XX
KW   Polychlorinated biphenyls; PCBs; dechlorinating activity; ds.
XX
OS   Unidentified.
XX
PN   WO2003065011-A2.
XX
PD   07-AUG-2003.
XX
PF   03-FEB-2003; 2003WO-US003202.
XX
PR   01-FEB-2002; 2002US-0353134P.
XX
PA   (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX
PI   Sowers KR,  May HD;
XX
DR   WPI; 2003-636818/60.
XX
PT   Stimulation of polychlorinated biphenyl dechlorinating bacteria comprises
PT   contacting polychlorinated biphenyl dechlorinating bacteria with
PT   stimulant having polyhalogenated ethene(s).
XX
PS   Disclosure; Fig 4; 41pp; English.
XX
CC   The present invention relates to compositions and methods for
CC   bioremediation of polychlorinated biphenyls (PCBs) using dechlorinating
CC   microorganisms grown in the presence of stimulating halogenated
CC   hydrocarbons and polyhalogenated ethenes. Polyhalogenated ethenes are
CC   used to stimulate the growth and dechlorinating activity of PCB
CC   dechlorinating bacteria in a contaminated soil or sediment. The present
CC   sequence is 16S ribosomal subunit DNA
XX
SQ   Sequence 336 BP; 76 A; 83 C; 97 G; 80 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 9;  Length 336;
  Best Local Similarity   100.0%;  Pred. No. 0.00072;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        323 ACAAGGCCCGAGAACGTATTCA 302


RESULT 3
AAD58049/c
ID   AAD58049 standard; DNA; 1014 BP.
XX
AC   AAD58049;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Dehalococcoides related family A 16S DHFA sequence.
XX
KW   16S rDNA; dechlorinating bacterial organism; ds.
XX
OS   Unidentified.
XX
PN   WO2003064695-A1.
XX
PD   07-AUG-2003.
XX
PF   30-JAN-2002; 2002WO-US003927.
XX
PR   30-JAN-2002; 2002WO-US003927.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Ebersole R,  Hendrickson E;
XX
DR   WPI; 2003-636804/60.
XX
PT   Novel isolated 16S rDNA sequence useful for forming probes and primers
PT   which are useful for identifying dechlorinating bacterial organism in
PT   various samples.
XX
PS   Claim 1; Page 99-100; 110pp; English.
XX
CC   The invention relates to an isolated 16S rDNA sequence indicative of a
CC   dechlorinating bacterial organism. The invention is useful for forming
CC   probes and primers which are useful for identifying dechlorinating
CC   bacterial organism in various samples. The method of the invention is
CC   useful for identifying a dechlorinating bacterial organism that is a
CC   member of a cell population or consortium. The isolated bacterial
CC   organism is useful for dechlorinating chlorinated compounds which
CC   involves contacting a chlorinated compound with the organism.
CC   Oligonucleotide polymer of the invention is useful for separating sub-
CC   families of dechlorinating bacterial organism. The present sequence is
CC   Dehalococcoides related family A 16S DHFA sequence
XX
SQ   Sequence 1014 BP; 256 A; 238 C; 309 G; 211 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 8;  Length 1014;
  Best Local Similarity   100.0%;  Pred. No. 0.0007;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db       1004 ACAAGGCCCGAGAACGTATTCA 983


RESULT 4
AAH28398/c
ID   AAH28398 standard; rRNA; 1284 BP.
XX
AC   AAH28398;
XX
DT   11-SEP-2003  (revised)
DT   17-SEP-2001  (first entry)
XX
DE   Intergenic spacer between 16S and 23S rRNA genes of strain FML-12.
XX
KW   Intergenic spacer; Chlamydiaceae; 16S rRNA; 23S rRNA; Region A; Region B;
KW   chlamydial infection; ss.
XX
OS   Chlamydophila pneumoniae.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .537
FT                   /*tag=  b
FT                   /note= "Region A"
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```
FT   rRNA            1. .221
FT                   /*tag=  a
FT                   /note= "16S rRNA"
FT   misc_RNA        222. .444
FT                   /*tag=  c
FT                   /note= "intergenic spacer"
FT   rRNA            445. .1284
FT                   /*tag=  e
FT                   /note= "23S rRNA"
FT   rRNA            445. .1063
FT                   /*tag=  d
FT                   /note= "Domain I of 23S rRNA"
FT   misc_RNA        959. .1086
FT                   /*tag=  f
FT                   /note= "Region B"
XX
PN   US6261769-B1.
XX
PD   17-JUL-2001.
XX
PF   31-MAR-1998;   98US-00052333.
XX
PR   31-MAR-1998;   98US-00052333.
XX
PA   (USDA ) US SEC OF AGRIC.
XX
PI   Everett KDE,  Andersen AA;
XX
DR   WPI; 2001-440857/47.
XX
PT   New primers and probes derived from sequences of intergenic spacer
PT   between 16S and 23S genes and region of Domain I in 23S region of
PT   Chlamydiaceae, useful for assaying and identifying all strains of
PT   Chlamydiaceae.
XX
PS   Disclosure; Col 119-120; 89pp; English.
XX
CC   AAH28371-AAH28413 represent intergenic spacer target sequences, derived
CC   from Chlamydiaceae. The sequences comprise the intergenic spacer between
CC   the 16S and the 23S rRNA genes, including the far downstream end of the
CC   16S and the far upstream end of the 23S domain I flanking intergenic
CC   spacer (referred to as Region A), and secondarily, a 131 bp region in the
CC   3' end of Domain I (referred to as Region B). The sequences provide
CC   suitable target sequences for developing probes and primers which are
CC   useful for identifying and detecting Chlamydiaceae. The primers and
CC   probes can be used to identify the presence of Chlamydiaceae in a test
CC   sample, or to distinguish one strain from another, and for diagnosing
CC   chlamydial infections in humans and animals. (Updated on 11-SEP-2003 to
CC   standardise OS field)
XX
SQ   Sequence 1284 BP; 394 A; 216 C; 330 G; 344 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 4;  Length 1284;
  Best Local Similarity   100.0%;  Pred. No. 0.00069;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db         67 ACAAGGCCCGAGAACGTATTCA 46


RESULT 5
AAH28396/c
ID   AAH28396 standard; rRNA; 1284 BP.
XX
AC   AAH28396;
XX
DT   11-SEP-2003  (revised)
DT   17-SEP-2001  (first entry)
XX
DE   Intergenic spacer between 16S and 23S rRNA genes of strain CWL-029.
XX
KW   Intergenic spacer; Chlamydiaceae; 16S rRNA; 23S rRNA; Region A; Region B;
KW   chlamydial infection; ss.
XX
OS   Chlamydophila pneumoniae.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .537
FT                   /*tag=  b
FT                   /note= "Region A"
FT   rRNA            1. .221
FT                   /*tag=  a
FT                   /note= "16S rRNA"
FT   misc_RNA        222. .444
FT                   /*tag=  c
FT                   /note= "intergenic spacer"
FT   rRNA            445. .1284
FT                   /*tag=  e
FT                   /note= "23S rRNA"
FT   rRNA            445. .1063
FT                   /*tag=  d
FT                   /note= "Domain I of 23S rRNA"
FT   misc_RNA        959. .1086
FT                   /*tag=  f
FT                   /note= "Region B"
XX
PN   US6261769-B1.
XX
PD   17-JUL-2001.
XX
PF   31-MAR-1998;   98US-00052333.
XX
PR   31-MAR-1998;   98US-00052333.
XX
PA   (USDA ) US SEC OF AGRIC.
XX
PI   Everett KDE,  Andersen AA;
XX
DR   WPI; 2001-440857/47.
XX
PT   New primers and probes derived from sequences of intergenic spacer
PT   between 16S and 23S genes and region of Domain I in 23S region of
PT   Chlamydiaceae, useful for assaying and identifying all strains of
PT   Chlamydiaceae.
XX
PS   Disclosure; Col 113-116; 89pp; English.
XX
CC   AAH28371-AAH28413 represent intergenic spacer target sequences, derived
CC   from Chlamydiaceae. The sequences comprise the intergenic spacer between
CC   the 16S and the 23S rRNA genes, including the far downstream end of the
CC   16S and the far upstream end of the 23S domain I flanking intergenic
CC   spacer (referred to as Region A), and secondarily, a 131 bp region in the
CC   3' end of Domain I (referred to as Region B). The sequences provide
CC   suitable target sequences for developing probes and primers which are
CC   useful for identifying and detecting Chlamydiaceae. The primers and
CC   probes can be used to identify the presence of Chlamydiaceae in a test
CC   sample, or to distinguish one strain from another, and for diagnosing
CC   chlamydial infections in humans and animals. (Updated on 11-SEP-2003 to
CC   standardise OS field)
XX
SQ   Sequence 1284 BP; 394 A; 218 C; 329 G; 343 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 4;  Length 1284;
  Best Local Similarity   100.0%;  Pred. No. 0.00069;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db         67 ACAAGGCCCGAGAACGTATTCA 46


RESULT 6
AAH28401/c
ID   AAH28401 standard; rRNA; 1284 BP.
XX
```

```
AC   AAH28401;
XX
DT   11-SEP-2003  (revised)
DT   17-SEP-2001  (first entry)
XX
DE   Intergenic spacer between 16S and 23S rRNA genes of strain TW-183.
XX
KW   Intergenic spacer; Chlamydiaceae; 16S rRNA; 23S rRNA; Region A; Region B;
KW   chlamydial infection; ss.
XX
OS   Chlamydophila pneumoniae.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .537
FT                   /*tag=  b
FT                   /note= "Region A"
FT   rRNA            1. .221
FT                   /*tag=  a
FT                   /note= "16S rRNA"
FT   misc_RNA        222. .444
FT                   /*tag=  c
FT                   /note= "intergenic spacer"
FT   rRNA            445. .1284
FT                   /*tag=  e
FT                   /note= "23S rRNA"
FT   rRNA            445. .1063
FT                   /*tag=  d
FT                   /note= "Domain I of 23S rRNA"
FT   misc_RNA        959. .1086
FT                   /*tag=  f
FT                   /note= "Region B"
XX
PN   US6261769-B1.
XX
PD   17-JUL-2001.
XX
PF   31-MAR-1998;   98US-00052333.
XX
PR   31-MAR-1998;   98US-00052333.
XX
PA   (USDA ) US SEC OF AGRIC.
XX
PI   Everett KDE,  Andersen AA;
XX
DR   WPI; 2001-440857/47.
XX
PT   New primers and probes derived from sequences of intergenic spacer
PT   between 16S and 23S genes and region of Domain I in 23S region of
PT   Chlamydiaceae, useful for assaying and identifying all strains of
PT   Chlamydiaceae.
XX
PS   Disclosure; Col 125-128; 89pp; English.
XX
CC   AAH28371-AAH28413 represent intergenic spacer target sequences, derived
CC   from Chlamydiaceae. The sequences comprise the intergenic spacer between
CC   the 16S and the 23S rRNA genes, including the far downstream end of the
CC   16S and the far upstream end of the 23S domain I flanking intergenic
CC   spacer (referred to as Region A), and secondarily, a 131 bp region in the
CC   3' end of Domain I (referred to as Region B). The sequences provide
CC   suitable target sequences for developing probes and primers which are
CC   useful for identifying and detecting Chlamydiaceae. The primers and
CC   probes can be used to identify the presence of Chlamydiaceae in a test
CC   sample, or to distinguish one strain from another, and for diagnosing
CC   chlamydial infections in humans and animals. (Updated on 11-SEP-2003 to
CC   standardise OS field)
XX
SQ   Sequence 1284 BP; 394 A; 216 C; 330 G; 344 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 22;  DB 4;  Length 1284;
  Best Local Similarity  100.0%;  Pred. No. 0.00069;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
                ||||||||||||||||||||||
Db         67 ACAAGGCCCGAGAACGTATTCA 46


RESULT 7
AAH28397/c
ID   AAH28397 standard; rRNA; 1284 BP.
XX
AC   AAH28397;
XX
DT   11-SEP-2003  (revised)
DT   17-SEP-2001  (first entry)
XX
DE   Intergenic spacer between 16S and 23S rRNA genes of strain CWL-1011.
XX
KW   Intergenic spacer; Chlamydiaceae; 16S rRNA; 23S rRNA; Region A; Region B;
KW   chlamydial infection; ss.
XX
OS   Chlamydophila pneumoniae.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .537
FT                   /*tag=  b
FT                   /note= "Region A"
FT   rRNA            1. .221
FT                   /*tag=  a
FT                   /note= "16S rRNA"
FT   misc_RNA        222. .444
FT                   /*tag=  c
FT                   /note= "intergenic spacer"
FT   rRNA            445. .1284
FT                   /*tag=  e
FT                   /note= "23S rRNA"
FT   rRNA            445. .1063
FT                   /*tag=  d
FT                   /note= "Domain I of 23S rRNA"
FT   misc_RNA        959. .1086
FT                   /*tag=  f
FT                   /note= "Region B"
XX
PN   US6261769-B1.
XX
PD   17-JUL-2001.
XX
PF   31-MAR-1998;   98US-00052333.
XX
PR   31-MAR-1998;   98US-00052333.
XX
PA   (USDA ) US SEC OF AGRIC.
XX
PI   Everett KDE,  Andersen AA;
XX
DR   WPI; 2001-440857/47.
XX
PT   New primers and probes derived from sequences of intergenic spacer
PT   between 16S and 23S genes and region of Domain I in 23S region of
PT   Chlamydiaceae, useful for assaying and identifying all strains of
PT   Chlamydiaceae.
XX
PS   Disclosure; Col 115-118; 89pp; English.
XX
CC   AAH28371-AAH28413 represent intergenic spacer target sequences, derived
CC   from Chlamydiaceae. The sequences comprise the intergenic spacer between
CC   the 16S and the 23S rRNA genes, including the far downstream end of the
CC   16S and the far upstream end of the 23S domain I flanking intergenic
CC   spacer (referred to as Region A), and secondarily, a 131 bp region in the
CC   3' end of Domain I (referred to as Region B). The sequences provide
CC   suitable target sequences for developing probes and primers which are
CC   useful for identifying and detecting Chlamydiaceae. The primers and
CC   probes can be used to identify the presence of Chlamydiaceae in a test
CC   sample, or to distinguish one strain from another, and for diagnosing
CC   chlamydial infections in humans and animals. (Updated on 11-SEP-2003 to
CC   standardise OS field)
```

```
XX
SQ   Sequence 1284 BP; 392 A; 218 C; 331 G; 343 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 4;  Length 1284;
  Best Local Similarity   100.0%;  Pred. No. 0.00069;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db         67 ACAAGGCCCGAGAACGTATTCA 46


RESULT 8
AAH28399/c
ID   AAH28399 standard; rRNA; 1284 BP.
XX
AC   AAH28399;
XX
DT   11-SEP-2003  (revised)
DT   17-SEP-2001  (first entry)
XX
DE   Intergenic spacer between 16S and 23S rRNA genes of strain FML-16.
XX
KW   Intergenic spacer; Chlamydiaceae; 16S rRNA; 23S rRNA; Region A; Region B;
KW   chlamydial infection; ss.
XX
OS   Chlamydophila pneumoniae.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .537
FT                   /*tag=  b
FT                   /note= "Region A"
FT   rRNA            1. .221
FT                   /*tag=  a
FT                   /note= "16S rRNA"
FT   misc_RNA        222. .444
FT                   /*tag=  c
FT                   /note= "intergenic spacer"
FT   rRNA            445. .1284
FT                   /*tag=  e
FT                   /note= "23S rRNA"
FT   rRNA            445. .1063
FT                   /*tag=  d
FT                   /note= "Domain I of 23S rRNA"
FT   misc_RNA        959. .1086
FT                   /*tag=  f
FT                   /note= "Region B"
XX
PN   US6261769-B1.
XX
PD   17-JUL-2001.
XX
PF   31-MAR-1998;   98US-00052333.
XX
PR   31-MAR-1998;   98US-00052333.
XX
PA   (USDA ) US SEC OF AGRIC.
XX
PI   Everett KDE,  Andersen AA;
XX
DR   WPI; 2001-440857/47.
XX
PT   New primers and probes derived from sequences of intergenic spacer
PT   between 16S and 23S genes and region of Domain I in 23S region of
PT   Chlamydiaceae, useful for assaying and identifying all strains of
PT   Chlamydiaceae.
XX
PS   Disclosure; Col 121-122; 89pp; English.
XX
CC   AAH28371-AAH28413 represent intergenic spacer target sequences, derived
CC   from Chlamydiaceae. The sequences comprise the intergenic spacer between
CC   the 16S and the 23S rRNA genes, including the far downstream end of the
CC   16S and the far upstream end of the 23S domain I flanking intergenic
CC   spacer (referred to as Region A), and secondarily, a 131 bp region in the
CC   3' end of Domain I (referred to as Region B). The sequences provide
CC   suitable target sequences for developing probes and primers which are
CC   useful for identifying and detecting Chlamydiaceae. The primers and
CC   probes can be used to identify the presence of Chlamydiaceae in a test
CC   sample, or to distinguish one strain from another, and for diagnosing
CC   chlamydial infections in humans and animals. (Updated on 11-SEP-2003 to
CC   standardise OS field)
XX
SQ   Sequence 1284 BP; 394 A; 216 C; 330 G; 344 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 4;  Length 1284;
  Best Local Similarity   100.0%;  Pred. No. 0.00069;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db         67 ACAAGGCCCGAGAACGTATTCA 46


RESULT 9
AAC62240/c
ID   AAC62240 standard; DNA; 1335 BP.
XX
AC   AAC62240;
XX
DT   19-MAR-2001  (first entry)
XX
DE   A 16S rDNA sequence indicative of a chlorinating bacterial strain.
XX
KW   16S rDNA; dechlorinating activity; chlorinated compound; vinyl chloride;
KW   carbontetrachloride; tetrachloroethane; chloroform; dichloromethane;
KW   trichloroethane; dichloroethylene; chlorinating bacteria; ss.
XX
OS   Dehalococcoides ethenogenes.
XX
PN   WO200063443-A2.
XX
PD   26-OCT-2000.
XX
PF   13-APR-2000; 2000WO-US009883.
XX
PR   15-APR-1999;   99US-0129511P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Hendrickson ER,  Ebersole RC;
XX
DR   WPI; 2001-024581/03.
XX
PT   New 16S rDNA profile derived from Dehalococcoides ethenogenes and
PT   indicative of a dechlorinating bacterial strain.
XX
PS   Claim 1; Page 47-48; 55pp; English.
XX
CC   The present sequence represents the 16S rDNA profile of Dehalococcoides
CC   ethenogenes strain STF, isolated from soil surrounding an industrial
CC   site. The 16S rDNA profile is linked to dechlorinating activity.
CC   Bacterial strain comprising the 16S rDNA sequence of the invention are
CC   useful for the dechlorination of chlorinated compounds such as
CC   carbontetrachloride, tetrachloroethane, chloroform, dichloromethane,
CC   trichloroethane, dichloroethylene, vinyl chloride, and chloroaromatics.
CC   The 16S rDNA sequence is also useful for identification of new
CC   chlorinating bacteria, as well as sub-typing strains of Dehalococcoides
CC   ethenogenes
XX
SQ   Sequence 1335 BP; 348 A; 288 C; 403 G; 296 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 4;  Length 1335;
  Best Local Similarity   100.0%;  Pred. No. 0.00069;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
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                    ||||||||||||||||||||
Db       1322 ACAAGGCCCGAGAACGTATTCA 1301


RESULT 10
AAD57959/c
ID   AAD57959 standard; DNA; 1377 BP.
XX
AC   AAD57959;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Dehalococcoides ethenogenes strain DAB 16S rDNA (DHE-DAB).
XX
KW   16S rDNA; dechlorinating bacterial organism; ds.
XX
OS   Dehalococcoides ethenogenes.
XX
PN   WO2003064695-A1.
XX
PD   07-AUG-2003.
XX
PF   30-JAN-2002; 2002WO-US003927.
XX
PR   30-JAN-2002; 2002WO-US003927.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Ebersole R,  Hendrickson E;
XX
DR   WPI; 2003-636804/60.
XX
PT   Novel isolated 16S rDNA sequence useful for forming probes and primers
PT   which are useful for identifying dechlorinating bacterial organism in
PT   various samples.
XX
PS   Claim 31; Fig 1; 110pp; English.
XX
CC   The invention relates to an isolated 16S rDNA sequence indicative of a
CC   dechlorinating bacterial organism. The invention is useful for forming
CC   probes and primers which are useful for identifying dechlorinating
CC   bacterial organism in various samples. The method of the invention is
CC   useful for identifying a dechlorinating bacterial organism that is a
CC   member of a cell population or consortium. The isolated bacterial
CC   organism is useful for dechlorinating chlorinated compounds which
CC   involves contacting a chlorinated compound with the organism.
CC   Oligonucleotide polymer of the invention is useful for separating sub-
CC   families of dechlorinating bacterial organism. The present sequence is
CC   Dehalococcoides ethenogenes 16S rDNA
XX
SQ   Sequence 1377 BP; 357 A; 299 C; 415 G; 306 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 8;  Length 1377;
  Best Local Similarity   100.0%;  Pred. No. 0.00069;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db       1321 ACAAGGCCCGAGAACGTATTCA 1300


RESULT 11
AAD57957/c
ID   AAD57957 standard; DNA; 1377 BP.
XX
AC   AAD57957;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Dehalococcoides ethenogenes strain PL 16S rDNA (DHE-PL).
XX
KW   16S rDNA; dechlorinating bacterial organism; ds.
XX
OS   Dehalococcoides ethenogenes.
XX
PN   WO2003064695-A1.
XX
PD   07-AUG-2003.
XX
PF   30-JAN-2002; 2002WO-US003927.
XX
PR   30-JAN-2002; 2002WO-US003927.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Ebersole R,  Hendrickson E;
XX
DR   WPI; 2003-636804/60.
XX
PT   Novel isolated 16S rDNA sequence useful for forming probes and primers
PT   which are useful for identifying dechlorinating bacterial organism in
PT   various samples.
XX
PS   Claim 31; Fig 1; 110pp; English.
XX
CC   The invention relates to an isolated 16S rDNA sequence indicative of a
CC   dechlorinating bacterial organism. The invention is useful for forming
CC   probes and primers which are useful for identifying dechlorinating
CC   bacterial organism in various samples. The method of the invention is
CC   useful for identifying a dechlorinating bacterial organism that is a
CC   member of a cell population or consortium. The isolated bacterial
CC   organism is useful for dechlorinating chlorinated compounds which
CC   involves contacting a chlorinated compound with the organism.
CC   Oligonucleotide polymer of the invention is useful for separating sub-
CC   families of dechlorinating bacterial organism. The present sequence is
CC   Dehalococcoides ethenogenes 16S rDNA
XX
SQ   Sequence 1377 BP; 361 A; 298 C; 412 G; 305 T; 0 U; 1 Other;

  Query Match             100.0%;  Score 22;  DB 8;  Length 1377;
  Best Local Similarity   100.0%;  Pred. No. 0.00069;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db       1321 ACAAGGCCCGAGAACGTATTCA 1300


RESULT 12
AAD57961/c
ID   AAD57961 standard; DNA; 1377 BP.
XX
AC   AAD57961;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Dehalococcoides ethenogenes strain DLL 16S rDNA (DHE-DLL).
XX
KW   16S rDNA; dechlorinating bacterial organism; ds.
XX
OS   Dehalococcoides ethenogenes.
XX
PN   WO2003064695-A1.
XX
PD   07-AUG-2003.
XX
PF   30-JAN-2002; 2002WO-US003927.
XX
PR   30-JAN-2002; 2002WO-US003927.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Ebersole R,  Hendrickson E;
XX
DR   WPI; 2003-636804/60.
XX
```

PT Novel isolated 16S rDNA sequence useful for forming probes and primers
PT which are useful for identifying dechlorinating bacterial organism in
PT various samples.
XX
PS Claim 31; Fig 1; 110pp; English.
XX
CC The invention relates to an isolated 16S rDNA sequence indicative of a
CC dechlorinating bacterial organism. The invention is useful for forming
CC probes and primers which are useful for identifying dechlorinating
CC bacterial organism in various samples. The method of the invention is
CC useful for identifying a dechlorinating bacterial organism that is a
CC member of a cell population or consortium. The isolated bacterial
CC organism is useful for dechlorinating chlorinated compounds which
CC involves contacting a chlorinated compound with the organism.
CC Oligonucleotide polymer of the invention is useful for separating sub-
CC families of dechlorinating bacterial organism. The present sequence is
CC Dehalococcoides ethenogenes 16S rDNA
XX
SQ Sequence 1377 BP; 360 A; 300 C; 414 G; 303 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 8; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAAGGCCCGAGAACGTATTCA 22
||||||||||||||||||||||
Db 1321 ACAAGGCCCGAGAACGTATTCA 1300

RESULT 13
AAD57960/c
ID AAD57960 standard; DNA; 1377 BP.
XX
AC AAD57960;
XX
DT 20-NOV-2003 (first entry)
XX
DE Dehalococcoides ethenogenes strain PIN 16S rDNA (DHE-PIN).
XX
KW 16S rDNA; dechlorinating bacterial organism; ds.
XX
OS Dehalococcoides ethenogenes.
XX
PN WO2003064695-A1.
XX
PD 07-AUG-2003.
XX
PF 30-JAN-2002; 2002WO-US003927.
XX
PR 30-JAN-2002; 2002WO-US003927.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Ebersole R, Hendrickson E;
XX
DR WPI; 2003-636804/60.
XX
PT Novel isolated 16S rDNA sequence useful for forming probes and primers
PT which are useful for identifying dechlorinating bacterial organism in
PT various samples.
XX
PS Claim 31; Fig 1; 110pp; English.
XX
CC The invention relates to an isolated 16S rDNA sequence indicative of a
CC dechlorinating bacterial organism. The invention is useful for forming
CC probes and primers which are useful for identifying dechlorinating
CC bacterial organism in various samples. The method of the invention is
CC useful for identifying a dechlorinating bacterial organism that is a
CC member of a cell population or consortium. The isolated bacterial
CC organism is useful for dechlorinating chlorinated compounds which
CC involves contacting a chlorinated compound with the organism.
CC Oligonucleotide polymer of the invention is useful for separating sub-
CC families of dechlorinating bacterial organism. The present sequence is
CC Dehalococcoides ethenogenes 16S rDNA
XX
SQ Sequence 1377 BP; 357 A; 299 C; 415 G; 306 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 8; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAAGGCCCGAGAACGTATTCA 22
||||||||||||||||||||||
Db 1321 ACAAGGCCCGAGAACGTATTCA 1300

RESULT 14
AAD57958/c
ID AAD57958 standard; DNA; 1378 BP.
XX
AC AAD57958;
XX
DT 20-NOV-2003 (first entry)
XX
DE Dehalococcoides ethenogenes strain V/SFD 16S rDNA (DHE-V/SFD).
XX
KW 16S rDNA; dechlorinating bacterial organism; ds.
XX
OS Dehalococcoides ethenogenes.
XX
PN WO2003064695-A1.
XX
PD 07-AUG-2003.
XX
PF 30-JAN-2002; 2002WO-US003927.
XX
PR 30-JAN-2002; 2002WO-US003927.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Ebersole R, Hendrickson E;
XX
DR WPI; 2003-636804/60.
XX
PT Novel isolated 16S rDNA sequence useful for forming probes and primers
PT which are useful for identifying dechlorinating bacterial organism in
PT various samples.
XX
PS Claim 31; Fig 1; 110pp; English.
XX
CC The invention relates to an isolated 16S rDNA sequence indicative of a
CC dechlorinating bacterial organism. The invention is useful for forming
CC probes and primers which are useful for identifying dechlorinating
CC bacterial organism in various samples. The method of the invention is
CC useful for identifying a dechlorinating bacterial organism that is a
CC member of a cell population or consortium. The isolated bacterial
CC organism is useful for dechlorinating chlorinated compounds which
CC involves contacting a chlorinated compound with the organism.
CC Oligonucleotide polymer of the invention is useful for separating sub-
CC families of dechlorinating bacterial organism. The present sequence is
CC Dehalococcoides ethenogenes 16S rDNA
XX
SQ Sequence 1378 BP; 361 A; 300 C; 413 G; 304 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 8; Length 1378;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAAGGCCCGAGAACGTATTCA 22
||||||||||||||||||||||
Db 1322 ACAAGGCCCGAGAACGTATTCA 1301

RESULT 15
AAC62244/c
ID AAC62244 standard; DNA; 1443 BP.

XX
AC AAC62244;
XX
DT 19-MAR-2001 (first entry)
XX
DE A 16S rDNA sequence indicative of a chlorinating bacterial strain.
XX
KW 16S rDNA; dechlorinating activity; chlorinated compound; vinyl chloride;
KW carbontetrachloride; tetrachloroethane; chloroform; dichloromethane;
KW trichloroethane; dichloroethylene; chlorinating bacteria; ss.
XX
OS Dehalococcoides ethenogenes.
XX
PN WO200063443-A2.
XX
PD 26-OCT-2000.
XX
PF 13-APR-2000; 2000WO-US009883.
XX
PR 15-APR-1999; 99US-0129511P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Hendrickson ER, Ebersole RC;
XX
DR WPI; 2001-024581/03.
XX
PT New 16S rDNA profile derived from Dehalococcoides ethenogenes and
PT indicative of a dechlorinating bacterial strain.
XX
PS Example 2; Page 49-50; 55pp; English.
XX
CC The present sequence represents the 16S rDNA profile of Dehalococcoides
CC ethenogenes strain 195. The 16S rDNA profile is linked to dechlorinating
CC activity. Bacterial strain comprising the 16S rDNA sequence of the
CC invention are useful for the dechlorination of chlorinated compounds such
CC as carbontetrachloride, tetrachloroethane, chloroform, dichloromethane,
CC trichloroethane, dichloroethylene, vinyl chloride, and chloroaromatics.
CC The 16S rDNA sequence is also useful for identification of new
CC chlorinating bacteria, as well as sub-typing strains of Dehalococcoides
CC ethenogenes
XX
SQ Sequence 1443 BP; 379 A; 306 C; 443 G; 314 T; 0 U; 1 Other;

Query Match 100.0%; Score 22; DB 4; Length 1443;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAAGGCCCGAGAACGTATTCA 22
||||||||||||||||||||||
Db 1329 ACAAGGCCCGAGAACGTATTCA 1308

Search completed: August 4, 2004, 06:43:37
Job time : 182.771 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 06:43:54 ; Search time 208.988 Seconds
(without alignments)
247.629 Million cell updates/sec

Title: US-09-940-860-4
Perfect score: 21
Sequence: 1 gtgccagcagcagcggtaata 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4754066 seqs, 1232178907 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9508132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_New:*
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6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq2:*
8: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq3:*
9: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	17	81.0	1542	8	US-10-864-684-581	Sequence 581, App
c	2	17	81.0	2838	1	PCT-US03-41761-45189	Sequence 45189, A
c	3	17	81.0	2838	1	PCT-US03-41761-45189	Sequence 45189, A
c	4	17	81.0	2838	1	PCT-US03-41766A-45189	Sequence 45189, A
	5	16	76.2	783	1	PCT-US03-36229-174	Sequence 174, App
	6	16	76.2	783	1	PCT-US04-17686-2493	Sequence 2493, Ap
	7	16	76.2	815	6	US-10-425-115-47421	Sequence 47421, A
c	8	16	76.2	830	6	US-10-425-115-79433	Sequence 79433, A
	9	16	76.2	1119	6	US-10-669-143-12	Sequence 12, Appl
	10	16	76.2	1119	7	US-10-835-208-10	Sequence 10, Appl
	11	16	76.2	1647	1	PCT-US04-05092-48	Sequence 48, Appl
c	12	16	76.2	109725	7	US-10-767-471-10719	Sequence 10719, A
c	13	15	71.4	201	6	US-10-425-115-139088	Sequence 139088,
c	14	15	71.4	213	1	PCT-US04-12047-347	Sequence 347, App
c	15	15	71.4	260	6	US-10-425-115-49000	Sequence 49000, A
c	16	15	71.4	300	6	US-10-425-115-44757	Sequence 44757, A
	17	15	71.4	526	6	US-10-425-115-139649	Sequence 139649,
c	18	15	71.4	717	6	US-10-425-115-152690	Sequence 152690,
c	19	15	71.4	748	6	US-10-425-115-171414	Sequence 171414,
	20	15	71.4	837	6	US-10-425-115-146825	Sequence 146825,
	21	15	71.4	863	6	US-10-425-115-146920	Sequence 146920,
	22	15	71.4	923	7	US-10-767-701-11322	Sequence 11322, A
c	23	15	71.4	1083	1	PCT-US04-02974-43	Sequence 43, Appl
c	24	15	71.4	1083	7	US-10-770-668-43	Sequence 43, Appl
	25	15	71.4	1126	1	PCT-US03-41761-34028	Sequence 34028, A
	26	15	71.4	1126	1	PCT-US03-41761-34028	Sequence 34028, A
	27	15	71.4	1126	1	PCT-US03-41766A-34028	Sequence 34028, A
c	28	15	71.4	1167	1	PCT-US04-07467-211	Sequence 211, App
	29	15	71.4	1205	6	US-10-425-115-100996	Sequence 100996,
c	30	15	71.4	1343	6	US-10-425-115-179268	Sequence 179268,
c	31	15	71.4	1636	7	US-10-796-174-56	Sequence 56, Appl
c	32	15	71.4	1739	6	US-10-425-115-14642	Sequence 14642, A
c	33	15	71.4	1751	1	PCT-US04-12706-29	Sequence 29, Appl
c	34	15	71.4	1751	7	US-10-830-828-29	Sequence 29, Appl
	35	15	71.4	2039	7	US-10-491-468-79	Sequence 79, Appl
c	36	15	71.4	3770	1	PCT-US04-11193-9	Sequence 9, Appli
c	37	15	71.4	3884	6	US-10-127-823A-145	Sequence 145, App
c	38	15	71.4	3884	7	US-10-152-372-145	Sequence 145, App
c	39	15	71.4	3884	7	US-10-123-155-145	Sequence 145, App
c	40	15	71.4	3884	8	US-10-143-117-145	Sequence 145, App
c	41	15	71.4	3884	8	US-10-143-117-145	Sequence 145, App
c	42	15	71.4	5337	7	US-10-852-074-11	Sequence 11, Appl
	43	15	71.4	17777	8	US-10-868-184A-5663	Sequence 5663, Ap
	44	15	71.4	17777	8	US-10-868-184-5663	Sequence 5663, Ap
c	45	14	66.7	78	1	PCT-US03-41269-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-10-864-684-581/c
; Sequence 581, Application US/10864684
; GENERAL INFORMATION:
; APPLICANT: Scarlato, Vincenzo
; APPLICANT: Masignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Neisserial Antigens
; FILE REFERENCE: CHIR0160
; CURRENT APPLICATION NUMBER: US/10/864,684
; CURRENT FILING DATE: 2004-06-08
; NUMBER OF SEQ ID NOS: 1168
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 581
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-864-684-581

Query Match 81.0%; Score 17; DB 8; Length 1542;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 GCCAGCAGCAGCGGTAA 19
              |||||||||||||||||
Db       1148 GCCAGCAGCAGCGGTAA 1132
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RESULT 2
PCT-US03-41761-45189/c
; Sequence 45189, Application PC/TUS0341761
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: CHARTERIS, Paul
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; TITLE OF INVENTION: COMPOSITIONS, METHODS, AND SYSTEMS FOR INFERRING BOVINE BREED
; FILE REFERENCE: MMI1150WO
; CURRENT APPLICATION NUMBER: PCT/US03/41761
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922

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;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 45189
;   LENGTH: 2838
;   TYPE: DNA
;   ORGANISM: Bovine  19866880933064
PCT-US03-41761-45189

  Query Match             81.0%;  Score 17;  DB 1;  Length 2838;
  Best Local Similarity   100.0%;  Pred. No. 9.7;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGT 17
              |||||||||||||||||
Db       2268 GTGCCAGCAGCAGCGGT 2252


RESULT 3
PCT-US03-41761-45189/c
; Sequence 45189, Application PC/TUS0341761
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  CHARTERIS, Paul
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  TITLE OF INVENTION: COMPOSITIONS, METHODS, AND SYSTEMS FOR INFERRING BOVINE BREED
;  FILE REFERENCE: MMI1150WO
;  CURRENT APPLICATION NUMBER: PCT/US03/41761
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 45189
;   LENGTH: 2838
;   TYPE: DNA
;   ORGANISM: Bovine  19866880933064
PCT-US03-41761-45189

  Query Match             81.0%;  Score 17;  DB 1;  Length 2838;
  Best Local Similarity   100.0%;  Pred. No. 9.7;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGT 17
              |||||||||||||||||
Db       2268 GTGCCAGCAGCAGCGGT 2252


RESULT 4
PCT-US03-41766A-45189/c
; Sequence 45189, Application PC/TUS0341766A
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS, METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100WO
;  CURRENT APPLICATION NUMBER: PCT/US03/41766A
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 45189
;   LENGTH: 2838
;   TYPE: DNA
;   ORGANISM: Bovine  19866880933064
PCT-US03-41766A-45189

  Query Match             81.0%;  Score 17;  DB 1;  Length 2838;
  Best Local Similarity   100.0%;  Pred. No. 9.7;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGT 17
              |||||||||||||||||
Db       2268 GTGCCAGCAGCAGCGGT 2252


RESULT 5
PCT-US03-36229-174
; Sequence 174, Application PC/TUS0336229
; GENERAL INFORMATION:
;  APPLICANT: Nura Inc
;  TITLE OF INVENTION: Nuclear Receptor-Based Diagnostic,
;  TITLE OF INVENTION:  Therapeutic and Screening Methods
;  FILE REFERENCE: 50001/014WO2
;  CURRENT APPLICATION NUMBER: PCT/US03/36229
;  CURRENT FILING DATE:  2003-11-12
;  PRIOR APPLICATION NUMBER: 60/426,305
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 198
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 174
;   LENGTH: 783
;   TYPE: DNA
;   ORGANISM: Mus musculus
PCT-US03-36229-174

  Query Match             76.2%;  Score 16;  DB 1;  Length 783;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGG 16
              ||||||||||||||||
Db        129 GTGCCAGCAGCAGCGG 144


RESULT 6
PCT-US04-17686-2493
; Sequence 2493, Application PC/TUS0417686
; GENERAL INFORMATION:
;  APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY
;  APPLICANT:  THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES, CENTERS
;  APPLICANT:  FOR DISEASE CONTROL AND PREVENTION
;  TITLE OF INVENTION: PNI MICROARRAY AND USES
;  FILE REFERENCE: 14114.0375P1
;  CURRENT APPLICATION NUMBER: PCT/US04/17686
;  CURRENT FILING DATE:  2004-06-21
;  PRIOR APPLICATION NUMBER: 60/475,915
;  PRIOR FILING DATE: 2003-06-04
;  NUMBER OF SEQ ID NOS: 3085
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2493
;   LENGTH: 783
;   TYPE: DNA
;   ORGANISM: Mus musculus
PCT-US04-17686-2493

  Query Match             76.2%;  Score 16;  DB 1;  Length 783;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGG 16
              ||||||||||||||||
Db        129 GTGCCAGCAGCAGCGG 144


RESULT 7
US-10-425-115-47421
; Sequence 47421, Application US/10425115
; GENERAL INFORMATION:
```

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 47421
; LENGTH: 815
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(815)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_143255C.1
US-10-425-115-47421

Query Match 76.2%; Score 16; DB 6; Length 815;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCCAGCAGCAGCGGTA 18
||||||||||||||||
Db 552 GCCAGCAGCAGCGGTA 567

RESULT 8
US-10-425-115-79433/c
; Sequence 79433, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 79433
; LENGTH: 830
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_172470C.1
US-10-425-115-79433

Query Match 76.2%; Score 16; DB 6; Length 830;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCCAGCAGCAGCGGTA 18
||||||||||||||||
Db 822 GCCAGCAGCAGCGGTA 807

RESULT 9
US-10-669-143-12
; Sequence 12, Application US/10669143
; GENERAL INFORMATION:
; APPLICANT: William Matthews
; APPLICANT: Mark Moore
; APPLICANT: Russell Phillips
; APPLICANT: Michael V. Wiles
; APPLICANT: Thadd C. Reeder
; APPLICANT: Robert G. Wisotzkey
; APPLICANT: Keith D. Allen
; APPLICANT: Helen Baribault
; APPLICANT: Thomas J. Brennan
; APPLICANT: Catherine Guenther
; APPLICANT: Robert Klein
; APPLICANT: Christopher J. Kirk
; APPLICANT: Simon X. Xie
; APPLICANT: Qin Zhang
; APPLICANT: Agnes Choppin
; TITLE OF INVENTION: Targeted Gene Disruptions, Compositions
; TITLE OF INVENTION: and Methods Related Thereto
; FILE REFERENCE: R-DB-13
; CURRENT APPLICATION NUMBER: US/10/669,143
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 60/413,647
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/413,666
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/413,653
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/413,646
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/413,625
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 60/413,639
; PRIOR FILING DATE: 2002-09-24
; NUMBER OF SEQ ID NOS: 237
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-669-143-12

Query Match 76.2%; Score 16; DB 6; Length 1119;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGG 16
||||||||||||||||
Db 161 GTGCCAGCAGCAGCGG 176

RESULT 10
US-10-835-208-10
; Sequence 10, Application US/10835208
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHORT HETERODIMER PARTNER-1 EXPRESSION
; FILE REFERENCE: ISPH-0593
; CURRENT APPLICATION NUMBER: US/10/835,208
; CURRENT FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: US/09/919,197
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (33)...(815)
US-10-835-208-10

Query Match 76.2%; Score 16; DB 7; Length 1119;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGG 16
||||||||||||||||
Db 161 GTGCCAGCAGCAGCGG 176

```
RESULT 11
PCT-US04-05092-48
; Sequence 48, Application PC/TUS0405092
; GENERAL INFORMATION:
;  APPLICANT: INCYTE CORPORATION; RAMKUMAR, Jayalaxmi;
;  APPLICANT:  MARQUIS, Joseph P.; SWARNAKAR, Anita;
;  APPLICANT:  CHAWLA, Narinder K.; TRAN, Uyen K.;
;  APPLICANT:  BECHA, Shanya ; LEE, Soo Yeun;
;  APPLICANT:  HAFALIA, April J.A.; RICHARDSON, Thomas;
;  APPLICANT:  KHARE, Reena; JIANG, Xin;
;  APPLICANT:  JACKSON, Alan; YANG, Junming;
;  APPLICANT:  GORVAD, Ann
;  TITLE OF INVENTION: KINASES AND PHOSPHATASES
;  FILE REFERENCE: PF-1643 PCT
;  CURRENT APPLICATION NUMBER: PCT/US04/05092
;  CURRENT FILING DATE:  2004-02-20
;  PRIOR APPLICATION NUMBER: US 60/449,059
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/456,932
;  PRIOR FILING DATE: 2003-03-19
;  PRIOR APPLICATION NUMBER: US 60/458,844
;  PRIOR FILING DATE: 2003-03-28
;  PRIOR APPLICATION NUMBER: US 60/461,678
;  PRIOR FILING DATE: 2003-04-09
;  PRIOR APPLICATION NUMBER: US 60/463,937
;  PRIOR FILING DATE: 2003-04-17
;  NUMBER OF SEQ ID NOS: 92
;  SOFTWARE: PERL Program
; SEQ ID NO 48
;   LENGTH: 1647
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 7523794CB1
PCT-US04-05092-48

  Query Match           76.2%;  Score 16;  DB 1;  Length 1647;
  Best Local Similarity  100.0%;  Pred. No. 31;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CCAGCAGCAGCGGTAA 19
              ||||||||||||||||
Db        856 CCAGCAGCAGCGGTAA 871


RESULT 12
US-10-767-471-10719/c
; Sequence 10719, Application US/10767471
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001505
;  CURRENT APPLICATION NUMBER: US/10/767,471
;  CURRENT FILING DATE:  2004-01-30
;  NUMBER OF SEQ ID NOS: 50231
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10719
;   LENGTH: 109725
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-767-471-10719

  Query Match           76.2%;  Score 16;  DB 7;  Length 109725;
  Best Local Similarity  100.0%;  Pred. No. 33;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 AGCAGCAGCGGTAATA 21
              ||||||||||||||||
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RESULT 13
US-10-425-115-139088/c
; Sequence 139088, Application US/10425115
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 139088
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_58330C.1
US-10-425-115-139088

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  Best Local Similarity  100.0%;  Pred. No. 97;
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RESULT 14
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; Sequence 347, Application PC/TUS0412047
; GENERAL INFORMATION:
;  APPLICANT: FIVE PRIME THERAPEUTICS, INC.
;  TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS OF
;  TITLE OF INVENTION:  THEIR USE
;  FILE REFERENCE: 08940.0021-00304
;  CURRENT APPLICATION NUMBER: PCT/US04/12047
;  CURRENT FILING DATE:  2004-05-04
;  NUMBER OF SEQ ID NOS: 1464
;  PRIOR APPLICATION NUMBER: US 60/463,732
;  PRIOR FILING DATE: 2003-04-18
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;  PRIOR FILING DATE: 2003-05-02
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;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: US 60/493,573
;  PRIOR FILING DATE: 2003-08-08
;  PRIOR APPLICATION NUMBER: US 60/493,577
;  PRIOR FILING DATE: 2003-08-08
;  PRIOR APPLICATION NUMBER: US 60/486,480
;  PRIOR FILING DATE: 2003-07-03
;  PRIOR APPLICATION NUMBER: US 60/486,446
;  PRIOR FILING DATE: 2003-07-03
;  PRIOR APPLICATION NUMBER: US 60/471,306
;  PRIOR FILING DATE: 2003-05-19
;  PRIOR APPLICATION NUMBER: US 60/471,336
;  PRIOR FILING DATE: 2003-05-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  SOFTWARE: PatentIn version 3.2
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;   ORGANISM: Homo sapiens
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RESULT 15
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; Sequence 49000, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 49000
; LENGTH: 260
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_144694C.1
US-10-425-115-49000

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Best Local Similarity 100.0%; Pred. No. 98;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        160 GTGCCAGCAGCAGCG 146
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OM nucleic - nucleic search, using sw model

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Title: US-09-940-860-4
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SUMMARIES

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3	21	100.0	5849	19	US-09-369-992C-1	Sequence 1, Appli
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5	19	90.5	116	23	US-09-540-235-4801	Sequence 4801, Ap
6	19	90.5	195	68	US-60-128-439-4848	Sequence 4848, Ap
7	19	90.5	239	23	US-09-540-235-5333	Sequence 5333, Ap
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9	19	90.5	287	68	US-60-128-439-2909	Sequence 2909, Ap
10	19	90.5	295	23	US-09-540-235-1015	Sequence 1015, Ap
11	19	90.5	295	68	US-60-128-439-1486	Sequence 1486, Ap
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19	19	90.5	343	68	US-60-128-439-1529	Sequence 1529, Ap
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25	19	90.5	364	23	US-09-540-235-2614	Sequence 2614, Ap
26	19	90.5	364	68	US-60-128-439-3929	Sequence 3929, Ap
27	19	90.5	370	68	US-60-128-439-3517	Sequence 3517, Ap
28	19	90.5	371	68	US-60-128-439-666	Sequence 666, App
29	19	90.5	372	23	US-09-540-235-3216	Sequence 3216, Ap
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34	19	90.5	380	23	US-09-540-235-4757	Sequence 4757, Ap
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ALIGNMENTS

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; Sequence 4, Application US/09940860
; GENERAL INFORMATION:
;  APPLICANT: Rothman, Richard
;  APPLICANT:  Majmudar, Maulik
;  TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
;  FILE REFERENCE: 01107.00185
;  CURRENT APPLICATION NUMBER: US/09/940,860
;  CURRENT FILING DATE:  2001-08-29
;  PRIOR APPLICATION NUMBER: 60/229,376
;  PRIOR FILING DATE: 2000-08-31
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic amplification primer
US-09-940-860-4

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RESULT 2
US-09-369-922-1
; Sequence 1, Application US/09369922
; GENERAL INFORMATION:
;  APPLICANT: Kara, Anna K.
;  APPLICANT:  Ting, Robert C.
;  APPLICANT:  Tham, Jill M.
;  APPLICANT:  Nelson, James S.
;  APPLICANT:  Tan, Theresa M.
;  TITLE OF INVENTION: Diagnosis of Plasmodium Infection by Analysis of
;  TITLE OF INVENTION:  Extrachromosomal Genetic Material
;  FILE REFERENCE: 64-99
;  CURRENT APPLICATION NUMBER: US/09/369,922
;  CURRENT FILING DATE:  1999-08-06
;  PRIOR APPLICATION NUMBER: PCT/IB98/00212
;  PRIOR FILING DATE: 1998-02-05
;  PRIOR APPLICATION NUMBER: AU PO9481/97
;  PRIOR FILING DATE: 1997-09-26
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;  PRIOR FILING DATE: 1997-04-21
;  PRIOR APPLICATION NUMBER: AU PO4953/97
;  PRIOR FILING DATE: 1997-02-06
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 5849
;   TYPE: DNA
;   ORGANISM: Plasmodium berghei
US-09-369-922-1

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RESULT 3
US-09-369-992C-1
; Sequence 1, Application US/09369992C
; GENERAL INFORMATION:
;  APPLICANT: Kara, Anna K.
;  APPLICANT:  Ting, Robert C.
;  APPLICANT:  Tham, Jill M.
;  APPLICANT:  Nelson, James S.
;  APPLICANT:  Tan, Theresa M.
;  TITLE OF INVENTION: Diagnosis of Parasites
;  FILE REFERENCE: 64-99
;  CURRENT APPLICATION NUMBER: US/09/369,992C
;  CURRENT FILING DATE:  1999-08-06
;  PRIOR APPLICATION NUMBER: PCT/IB98/00212
;  PRIOR FILING DATE: 1998-02-05
;  PRIOR APPLICATION NUMBER: AU PO9481/97
;  PRIOR FILING DATE: 1997-09-26
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;  PRIOR FILING DATE: 1997-04-21
;  PRIOR APPLICATION NUMBER: AU PO4953/97
;  PRIOR FILING DATE: 1997-02-06
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;   LENGTH: 5849
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;   ORGANISM: Plasmodium berghei
US-09-369-992C-1

  Query Match             100.0%;  Score 21;  DB 19;  Length 5849;
  Best Local Similarity   100.0%;  Pred. No. 5.5;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 4
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; Sequence 3619, Application US/60128439
; GENERAL INFORMATION:
;  APPLICANT: Fisher, Dane K.
;  APPLICANT: Lalgudi, Raghunath V.
;  TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
;  TITLE OF INVENTION: thereof
;  FILE REFERENCE: 38-21(15749)A
;  CURRENT APPLICATION NUMBER: US/60/128,439
;  CURRENT FILING DATE: 1999-04-06
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;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB190-049-Q1-E1-B2
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; Sequence 4801, Application US/09540235
; GENERAL INFORMATION:
;  APPLICANT:       Fisher, Dane K.
;  APPLICANT:  Lalgudi, Raghunath V.
;  TITLE OF INVENTION:       Nucleic Acid Sequences from Cyanidium caldarium and Uses
;  TITLE OF INVENTION:  thereof
;  FILE REFERENCE:       38-21(15749)B
;  CURRENT APPLICATION NUMBER: US/09/540,235
;  CURRENT FILING DATE:  2000-04-03
;  PRIOR APPLICATION NUMBER:       60/128,439
;  PRIOR FILING DATE:       1999-04-06
;  NUMBER OF SEQ ID NOS:       5674
; SEQ ID NO 4801
;   LENGTH: 116
;   TYPE: DNA
;   ORGANISM: Cyanidium caldarium
;   OTHER INFORMATION: Clone ID: LIB190-049-Q1-E1-B2
US-09-540-235-4801

  Query Match             90.5%;  Score 19;  DB 23;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 67;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAA 19
              |||||||||||||||||||
Db         96 GTGCCAGCAGCAGCGGTAA 114


RESULT 6
US-60-128-439-4848
; Sequence 4848, Application US/60128439
; GENERAL INFORMATION:
;  APPLICANT: Fisher, Dane K.
;  APPLICANT: Lalgudi, Raghunath V.
;  TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
;  TITLE OF INVENTION: thereof
;  FILE REFERENCE: 38-21(15749)A
;  CURRENT APPLICATION NUMBER: US/60/128,439
;  CURRENT FILING DATE: 1999-04-06
;  NUMBER OF SEQ ID NOS: 5661
; SEQ ID NO 4848
;   LENGTH: 195
;   TYPE: DNA
;   ORGANISM: Cyanidium caldarium
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB190-062-Q1-E1-E12
US-60-128-439-4848

  Query Match             90.5%;  Score 19;  DB 68;  Length 195;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAA 19
              |||||||||||||||||||
Db        114 GTGCCAGCAGCAGCGGTAA 132


RESULT 7
US-09-540-235-5333
; Sequence 5333, Application US/09540235
; GENERAL INFORMATION:
;  APPLICANT:       Fisher, Dane K.
;  APPLICANT:  Lalgudi, Raghunath V.
;  TITLE OF INVENTION:       Nucleic Acid Sequences from Cyanidium caldarium and Uses
;  TITLE OF INVENTION:  thereof
;  FILE REFERENCE:       38-21(15749)B
;  CURRENT APPLICATION NUMBER: US/09/540,235
;  CURRENT FILING DATE:  2000-04-03
;  PRIOR APPLICATION NUMBER:       60/128,439
;  PRIOR FILING DATE:       1999-04-06
;  NUMBER OF SEQ ID NOS:       5674
; SEQ ID NO 5333
;   LENGTH: 239
;   TYPE: DNA
;   ORGANISM: Cyanidium caldarium
;   OTHER INFORMATION: Clone ID: LIB190-062-Q1-E1-E12
US-09-540-235-5333

  Query Match             90.5%;  Score 19;  DB 23;  Length 239;
  Best Local Similarity   100.0%;  Pred. No. 62;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAA 19
              |||||||||||||||||||
Db        154 GTGCCAGCAGCAGCGGTAA 172


RESULT 8
US-60-128-439-3158
; Sequence 3158, Application US/60128439
; GENERAL INFORMATION:
;  APPLICANT: Fisher, Dane K.
;  APPLICANT: Lalgudi, Raghunath V.
;  TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
;  TITLE OF INVENTION: thereof
;  FILE REFERENCE: 38-21(15749)A
;  CURRENT APPLICATION NUMBER: US/60/128,439
;  CURRENT FILING DATE: 1999-04-06
;  NUMBER OF SEQ ID NOS: 5661
```

```
; SEQ ID NO 3158
;   LENGTH: 282
;   TYPE: DNA
;   ORGANISM: Cyanidium caldarium
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB190-043-Q1-E1-C12
US-60-128-439-3158

  Query Match             90.5%;  Score 19;  DB 68;  Length 282;
  Best Local Similarity   100.0%;  Pred. No. 61;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAA 19
              ||||||||||||||||||||
Db         51 GTGCCAGCAGCAGCGGTAA 69


RESULT 9
US-60-128-439-2909
; Sequence 2909, Application US/60128439
; GENERAL INFORMATION:
;  APPLICANT: Fisher, Dane K.
;  APPLICANT: Lalgudi, Raghunath V.
;  TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
;  TITLE OF INVENTION: thereof
;  FILE REFERENCE: 38-21(15749)A
;  CURRENT APPLICATION NUMBER: US/60/128,439
;  CURRENT FILING DATE: 1999-04-06
;  NUMBER OF SEQ ID NOS: 5661
; SEQ ID NO 2909
;   LENGTH: 287
;   TYPE: DNA
;   ORGANISM: Cyanidium caldarium
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB190-040-Q1-E1-B11
US-60-128-439-2909

  Query Match             90.5%;  Score 19;  DB 68;  Length 287;
  Best Local Similarity   100.0%;  Pred. No. 61;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAA 19
              ||||||||||||||||||||
Db         56 GTGCCAGCAGCAGCGGTAA 74


RESULT 10
US-09-540-235-1015
; Sequence 1015, Application US/09540235
; GENERAL INFORMATION:
;  APPLICANT:       Fisher, Dane K.
;  APPLICANT:  Lalgudi, Raghunath V.
;  TITLE OF INVENTION:       Nucleic Acid Sequences from Cyanidium caldarium and Uses
;  TITLE OF INVENTION:  thereof
;  FILE REFERENCE:       38-21(15749)B
;  CURRENT APPLICATION NUMBER: US/09/540,235
;  CURRENT FILING DATE:  2000-04-03
;  PRIOR APPLICATION NUMBER:       60/128,439
;  PRIOR FILING DATE:       1999-04-06
;  NUMBER OF SEQ ID NOS:       5674
; SEQ ID NO 1015
;   LENGTH: 295
;   TYPE: DNA
;   ORGANISM: Cyanidium caldarium
;   OTHER INFORMATION: Clone ID: LIB190-019-Q1-E1-H1
US-09-540-235-1015

  Query Match             90.5%;  Score 19;  DB 23;  Length 295;
  Best Local Similarity   100.0%;  Pred. No. 61;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAA 19
              ||||||||||||||||||||
Db        137 GTGCCAGCAGCAGCGGTAA 155


RESULT 11
US-60-128-439-1486
; Sequence 1486, Application US/60128439
; GENERAL INFORMATION:
;  APPLICANT: Fisher, Dane K.
;  APPLICANT: Lalgudi, Raghunath V.
;  TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
;  TITLE OF INVENTION: thereof
;  FILE REFERENCE: 38-21(15749)A
;  CURRENT APPLICATION NUMBER: US/60/128,439
;  CURRENT FILING DATE: 1999-04-06
;  NUMBER OF SEQ ID NOS: 5661
; SEQ ID NO 1486
;   LENGTH: 295
;   TYPE: DNA
;   ORGANISM: Cyanidium caldarium
;   FEATURE:
;   OTHER INFORMATION: unsure at all n locations
;   OTHER INFORMATION: Clone ID: LIB190-019-Q1-E1-H1
US-60-128-439-1486

  Query Match             90.5%;  Score 19;  DB 68;  Length 295;
  Best Local Similarity   100.0%;  Pred. No. 61;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAA 19
              ||||||||||||||||||||
Db        137 GTGCCAGCAGCAGCGGTAA 155


RESULT 12
US-09-540-235-4526
; Sequence 4526, Application US/09540235
; GENERAL INFORMATION:
;  APPLICANT:       Fisher, Dane K.
;  APPLICANT:  Lalgudi, Raghunath V.
;  TITLE OF INVENTION:       Nucleic Acid Sequences from Cyanidium caldarium and Uses
;  TITLE OF INVENTION:  thereof
;  FILE REFERENCE:       38-21(15749)B
;  CURRENT APPLICATION NUMBER: US/09/540,235
;  CURRENT FILING DATE:  2000-04-03
;  PRIOR APPLICATION NUMBER:       60/128,439
;  PRIOR FILING DATE:       1999-04-06
;  NUMBER OF SEQ ID NOS:       5674
; SEQ ID NO 4526
;   LENGTH: 300
;   TYPE: DNA
;   ORGANISM: Cyanidium caldarium
;   OTHER INFORMATION: Clone ID: LIB190-040-Q1-E1-B11
US-09-540-235-4526

  Query Match             90.5%;  Score 19;  DB 23;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 61;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTGCCAGCAGCAGCGGTAA 19
              ||||||||||||||||||||
Db         56 GTGCCAGCAGCAGCGGTAA 74


RESULT 13
US-09-540-235-3580
; Sequence 3580, Application US/09540235
; GENERAL INFORMATION:
;  APPLICANT:       Fisher, Dane K.
;  APPLICANT:  Lalgudi, Raghunath V.
;  TITLE OF INVENTION:       Nucleic Acid Sequences from Cyanidium caldarium and Uses
;  TITLE OF INVENTION:  thereof
;  FILE REFERENCE:       38-21(15749)B
;  CURRENT APPLICATION NUMBER: US/09/540,235
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; CURRENT FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/128,439
; PRIOR FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3580
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Cyanidium caldarium
; OTHER INFORMATION: Clone ID: LIB190-071-Q1-E1-G6
US-09-540-235-3580

Query Match 90.5%; Score 19; DB 23; Length 301;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGGTAA 19
||||||||||||||||||||
Db 160 GTGCCAGCAGCAGCGGTAA 178

RESULT 14
US-60-128-439-5580
; Sequence 5580, Application US/60128439
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Lalgudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
; TITLE OF INVENTION: thereof
; FILE REFERENCE: 38-21(15749)A
; CURRENT APPLICATION NUMBER: US/60/128,439
; CURRENT FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 5661
; SEQ ID NO 5580
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Cyanidium caldarium
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB190-071-Q1-E1-G6
US-60-128-439-5580

Query Match 90.5%; Score 19; DB 68; Length 301;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGGTAA 19
||||||||||||||||||||
Db 160 GTGCCAGCAGCAGCGGTAA 178

RESULT 15
US-09-540-235-4659
; Sequence 4659, Application US/09540235
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Lalgudi, Raghunath V.
; TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and Uses
; TITLE OF INVENTION: thereof
; FILE REFERENCE: 38-21(15749)B
; CURRENT APPLICATION NUMBER: US/09/540,235
; CURRENT FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/128,439
; PRIOR FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4659
; LENGTH: 302
; TYPE: DNA
; ORGANISM: Cyanidium caldarium
; OTHER INFORMATION: Clone ID: LIB190-043-Q1-E1-C12
US-09-540-235-4659

Query Match 90.5%; Score 19; DB 23; Length 302;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGGTAA 19
||||||||||||||||||||
Db 71 GTGCCAGCAGCAGCGGTAA 89

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Job time : 1918.07 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 06:01:54 ; Search time 37.9518 Seconds
(without alignments)
307.073 Million cell updates/sec

Title: US-09-940-860-4
Perfect score: 21
Sequence: 1 gtgccagcagcagcggtaata 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	16	76.2	426	4	US-09-252-991A-7151	Sequence 7151, Ap
	2	16	76.2	684	4	US-09-328-352-2320	Sequence 2320, Ap
c	3	16	76.2	783	4	US-09-252-991A-7428	Sequence 7428, Ap
	4	16	76.2	2541	4	US-09-252-991A-7209	Sequence 7209, Ap
c	5	16	76.2	3099	4	US-09-252-991A-7487	Sequence 7487, Ap
c	6	15	71.4	32	4	US-09-807-784B-11	Sequence 11, Appl
c	7	15	71.4	387	4	US-09-540-236-1498	Sequence 1498, Ap
c	8	15	71.4	398	4	US-09-621-976-9153	Sequence 9153, Ap
c	9	15	71.4	558	4	US-09-540-236-958	Sequence 958, App
	10	15	71.4	828	4	US-09-489-039A-4976	Sequence 4976, Ap
c	11	15	71.4	1050	4	US-09-252-991A-1269	Sequence 1269, Ap
c	12	15	71.4	1308	4	US-09-252-991A-1179	Sequence 1179, Ap
c	13	15	71.4	1575	3	US-08-639-294-1	Sequence 1, Appli
c	14	15	71.4	1575	4	US-09-861-034B-1	Sequence 1, Appli
c	15	15	71.4	1915	3	US-09-147-915-1	Sequence 1, Appli
c	16	15	71.4	2186	4	US-09-184-001-1	Sequence 1, Appli
c	17	15	71.4	2558	4	US-09-184-001-3	Sequence 3, Appli
	18	15	71.4	3762	4	US-09-489-039A-4926	Sequence 4926, Ap
c	19	15	71.4	62909	4	US-09-596-002-32	Sequence 32, Appl
	20	15	71.4	269223	4	US-09-596-002-41	Sequence 41, Appl
	21	15	71.4	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	22	15	71.4	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	23	14	66.7	15	3	US-09-275-850-25	Sequence 25, Appl
	24	14	66.7	17	1	US-08-554-612C-35	Sequence 35, Appl
c	25	14	66.7	39	3	US-08-721-458B-67	Sequence 67, Appl
	26	14	66.7	41	3	US-08-721-458B-68	Sequence 68, Appl
c	27	14	66.7	69	1	US-08-554-612C-37	Sequence 37, Appl
c	28	14	66.7	96	4	US-09-230-233A-4	Sequence 4, Appli
c	29	14	66.7	146	1	US-08-554-612C-48	Sequence 48, Appl
	30	14	66.7	225	4	US-09-621-976-538	Sequence 538, App
c	31	14	66.7	357	4	US-09-489-039A-909	Sequence 909, App
c	32	14	66.7	360	4	US-09-107-532A-181	Sequence 181, App
c	33	14	66.7	407	4	US-09-621-976-3580	Sequence 3580, Ap
	34	14	66.7	423	4	US-09-252-991A-606	Sequence 606, App
c	35	14	66.7	423	4	US-09-252-991A-9188	Sequence 9188, Ap
	36	14	66.7	423	4	US-09-252-991A-9323	Sequence 9323, Ap
	37	14	66.7	426	4	US-09-252-991A-14686	Sequence 14686, A
	38	14	66.7	429	4	US-09-252-991A-6653	Sequence 6653, Ap
	39	14	66.7	459	4	US-09-621-976-3656	Sequence 3656, Ap
	40	14	66.7	471	4	US-09-252-991A-10011	Sequence 10011, A
	41	14	66.7	471	4	US-09-489-039A-269	Sequence 269, App
	42	14	66.7	471	4	US-09-489-039A-1151	Sequence 1151, Ap
c	43	14	66.7	483	1	US-08-554-612C-15	Sequence 15, Appl
	44	14	66.7	495	4	US-09-252-991A-15946	Sequence 15946, A
	45	14	66.7	540	4	US-09-489-039A-156	Sequence 156, App

ALIGNMENTS

RESULT 1
US-09-252-991A-7151
; Sequence 7151, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7151
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (256)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-7151

Query Match 76.2%; Score 16; DB 4; Length 426;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GTGCCAGCAGCAGCGG 16
              ||||||||||||||||
Db         46 GTGCCAGCAGCAGCGG 61
```

RESULT 2
US-09-328-352-2320
; Sequence 2320, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 2320
; LENGTH: 684
; TYPE: DNA

; ORGANISM: Acinetobacter baumannii
US-09-328-352-2320

Query Match 76.2%; Score 16; DB 4; Length 684;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGCAGCAGCGGTAAT 20
||||||||||||||||
Db 170 CAGCAGCAGCGGTAAT 185

RESULT 3
US-09-252-991A-7428/c
; Sequence 7428, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7428
; LENGTH: 783
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (422)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-7428

Query Match 76.2%; Score 16; DB 4; Length 783;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGG 16
||||||||||||||||
Db 632 GTGCCAGCAGCAGCGG 617

RESULT 4
US-09-252-991A-7209
; Sequence 7209, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7209
; LENGTH: 2541
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (2058)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-7209

Query Match 76.2%; Score 16; DB 4; Length 2541;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGG 16
||||||||||||||||
Db 1848 GTGCCAGCAGCAGCGG 1863

RESULT 5
US-09-252-991A-7487/c
; Sequence 7487, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7487
; LENGTH: 3099
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1117)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-7487

Query Match 76.2%; Score 16; DB 4; Length 3099;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCCAGCAGCAGCGG 16
||||||||||||||||
Db 1327 GTGCCAGCAGCAGCGG 1312

RESULT 6
US-09-807-784B-11/c
; Sequence 11, Application US/09807784B
; Patent No. 6653118
; GENERAL INFORMATION:
; APPLICANT: Tanuma, Sei-ichi
; APPLICANT: Shiokawa, Daisuke
; TITLE OF INVENTION: No. 6653118el Deoxyribonuclease, Gene Encoding Thereof and Use Th
; FILE REFERENCE: 210792
; CURRENT APPLICATION NUMBER: US/09/807,784B
; CURRENT FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: JP 11-230870
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 11
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide designed to act as sense primer for
; OTHER INFORMATION: amplifying coding sequence of DNase II signal peptide.
US-09-807-784B-11

Query Match 71.4%; Score 15; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGCCAGCAGCAGCGG 16
|||||||||||||||

```
Db         32 TGCCAGCAGCAGCGG 18


RESULT 7
US-09-540-236-1498/c
; Sequence 1498, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
;  APPLICANT: Gary L. Breton et al.
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
;  TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 2709.2005-001
;  CURRENT APPLICATION NUMBER: US/09/540,236
;  CURRENT FILING DATE: 2000-04-04
;  NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 1498
;   LENGTH: 387
;   TYPE: DNA
;   ORGANISM: M.catarrhalis
US-09-540-236-1498

  Query Match             71.4%;  Score 15;  DB 4;  Length 387;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGCCAGCAGCAGCGG 16
              |||||||||||||||
Db        274 TGCCAGCAGCAGCGG 260


RESULT 8
US-09-621-976-9153/c
; Sequence 9153, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 9153
;   LENGTH: 398
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 320
;   OTHER INFORMATION: n=a, g, c or t
US-09-621-976-9153

  Query Match             71.4%;  Score 15;  DB 4;  Length 398;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGCCAGCAGCAGCGG 16
              |||||||||||||||
Db        126 TGCCAGCAGCAGCGG 112


RESULT 9
US-09-540-236-958/c
; Sequence 958, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
;  APPLICANT: Gary L. Breton et al.
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
;  TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 2709.2005-001
;  CURRENT APPLICATION NUMBER: US/09/540,236
;  CURRENT FILING DATE: 2000-04-04
;  NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 958
;   LENGTH: 558
;   TYPE: DNA
;   ORGANISM: M.catarrhalis
US-09-540-236-958

  Query Match             71.4%;  Score 15;  DB 4;  Length 558;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 AGCAGCAGCGGTAAT 20
              |||||||||||||||
Db        231 AGCAGCAGCGGTAAT 217


RESULT 10
US-09-489-039A-4976
; Sequence 4976, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 4976
;   LENGTH: 828
;   TYPE: DNA
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-4976

  Query Match             71.4%;  Score 15;  DB 4;  Length 828;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGCCAGCAGCAGCGG 16
              |||||||||||||||
Db        432 TGCCAGCAGCAGCGG 446


RESULT 11
US-09-252-991A-1269/c
; Sequence 1269, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 1269
;   LENGTH: 1050
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1269

  Query Match             71.4%;  Score 15;  DB 4;  Length 1050;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CCAGCAGCAGCGGTA 18
```

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                 ||||||||||||||||
Db        818 CCAGCAGCAGCGGTA 804


RESULT 12
US-09-252-991A-1179/c
; Sequence 1179, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 1179
;   LENGTH: 1308
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1179

  Query Match             71.4%;  Score 15;  DB 4;  Length 1308;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CCAGCAGCAGCGGTA 18
                ||||||||||||||||
Db        868 CCAGCAGCAGCGGTA 854


RESULT 13
US-08-639-294-1/c
; Sequence 1, Application US/08639294
; Patent No. 6265195
;  GENERAL INFORMATION:
;    APPLICANT:  Baker, Kevin P.
;    APPLICANT:  Baron, Will F.
;    TITLE OF INVENTION:  Human DNase II
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/639,294
;      FILING DATE:  25-Apr-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Johnston, Sean A.
;      REGISTRATION NUMBER:  35,910
;      REFERENCE/DOCKET NUMBER:  P1024
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-3562
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1575 base pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  DNA
US-08-639-294-1

  Query Match             71.4%;  Score 15;  DB 3;  Length 1575;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGCCAGCAGCAGCGG 16
                ||||||||||||||||
Db        106 TGCCAGCAGCAGCGG 92


RESULT 14
US-09-861-034B-1/c
; Sequence 1, Application US/09861034B
; Patent No. 6569429
;  GENERAL INFORMATION:
;       APPLICANT: Baker, Kevin P.
;                  Baron, Will F.
;       TITLE OF INVENTION: Human DNase II
;       NUMBER OF SEQUENCES: 10
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genentech, Inc.
;            STREET: 1 DNA Way
;            CITY: South San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94080
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WinPatin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/861,034B
;            FILING DATE: 18-May-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/639294
;            FILING DATE: 25-APR-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Johnston, Sean A.
;            REGISTRATION NUMBER: 35,910
;            REFERENCE/DOCKET NUMBER: P1024D1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650/225-3562
;            TELEFAX: 650/952-9881
;  INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1575 base pairs
;            TYPE: Nucleic Acid
;            STRANDEDNESS: Single
;            TOPOLOGY: Linear
;       MOLECULE TYPE: DNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-861-034B-1

  Query Match             71.4%;  Score 15;  DB 4;  Length 1575;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGCCAGCAGCAGCGG 16
                ||||||||||||||||
Db        106 TGCCAGCAGCAGCGG 92


RESULT 15
US-09-147-915-1/c
; Sequence 1, Application US/09147915A
; Patent No. 6184034
; GENERAL INFORMATION:
;  APPLICANT: Eastman, Alan
```

```
;  APPLICANT: Krieser, Ronald
;  TITLE OF INVENTION: Deoxyribonuclease II Proteins and cDNAs
;  FILE REFERENCE: DC-0097
;  CURRENT APPLICATION NUMBER: US/09/147,915A
;  CURRENT FILING DATE: 1999-03-23
;  EARLIER APPLICATION NUMBER: PCT/US97/18262
;  EARLIER FILING DATE: 1997-10-09
;  EARLIER APPLICATION NUMBER: 60/028,539
;  EARLIER FILING DATE: 1996-10-15
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1915
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-147-915-1

  Query Match             71.4%;  Score 15;  DB 3;  Length 1915;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGCCAGCAGCAGCGG 16
              |||||||||||||||
Db         88 TGCCAGCAGCAGCGG 74


Search completed: August  4, 2004, 09:23:34
Job time : 42.9518 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 05:41:25 ; Search time 1532.58 Seconds
(without alignments)
428.668 Million cell updates/sec

Title: US-09-940-860-3
Perfect score: 22
Sequence: 1 acaaggcccgagaacgtattca 22

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	16	72.7	213	9	AI212321	AI212321 x2g02a1.f
c	2	16	72.7	258	10	BF064383	BF064383 SWOvAFCAP
c	3	16	72.7	262	9	AI585049	AI585049 fb69g07.x
c	4	16	72.7	285	9	AI211182	AI211182 o0c05a1.f
c	5	16	72.7	324	9	AI381122	AI381122 SWOvAFCAP
c	6	16	72.7	348	9	AA497171	AA497171 fa01g09.s
	7	16	72.7	367	12	BI897005	BI897005 fk52e10.y
c	8	16	72.7	371	12	BI897004	BI897004 fk52e10.x
c	9	16	72.7	377	9	AA784579	AA784579 f1h09a1.f
c	10	16	72.7	445	12	BI896339	BI896339 fc43d02.x
c	11	16	72.7	445	12	BM156391	BM156391 fv18f06.y
c	12	16	72.7	448	12	BI533213	BI533213 fr79a06.x
c	13	16	72.7	452	12	BM102203	BM102203 fv14d10.x
c	14	16	72.7	458	12	BI896999	BI896999 fk50e03.x
c	15	16	72.7	459	12	BI708149	BI708149 fs42g04.x
c	16	16	72.7	466	12	BI866073	BI866073 ft98a01.x
c	17	16	72.7	471	12	BM102107	BM102107 fv13a06.x
c	18	16	72.7	477	9	AI087773	AI087773 SWOvAMCAQ
c	19	16	72.7	478	14	CB081772	CB081772 hk56e09.g
c	20	16	72.7	491	12	BI472977	BI472977 fr94c06.y
c	21	16	72.7	496	10	AW281793	AW281793 fj56h02.x
c	22	16	72.7	530	12	BI708185	BI708185 fs43c07.x
c	23	16	72.7	543	12	BI981155	BI981155 fu40d12.x
c	24	16	72.7	544	10	AW179661	AW179661 SWYD25CAU
c	25	16	72.7	545	9	AI353986	AI353986 zeh1247.s
c	26	16	72.7	568	9	AW077500	AW077500 fj35a03.y
c	27	16	72.7	569	12	BM024042	BM024042 fu69a03.y
c	28	16	72.7	591	12	BM070610	BM070610 fv02b01.y
c	29	16	72.7	622	14	CD014811	CD014811 hac25b10.
	30	16	72.7	672	12	BP176156	BP176156 BP176156
c	31	16	72.7	679	12	BP176155	BP176155 BP176155
	32	16	72.7	692	13	BU006325	BU006325 QGH10L09.
	33	16	72.7	702	14	CB678345	CB678345 OSJNEe16D
	34	16	72.7	759	28	BZ066995	BZ066995 ljt35d07.
	35	16	72.7	768	28	BZ067045	BZ067045 ljt35d07.
c	36	15	68.2	275	14	CD857812	CD857812 DH0AG5ZC0
c	37	15	68.2	295	14	CD856759	CD856759 DH0AG23ZD
c	38	15	68.2	304	14	CD857406	CD857406 DH0AG19ZD
c	39	15	68.2	313	14	CD857943	CD857943 DH0AG6ZF0
c	40	15	68.2	319	14	CD858282	CD858282 DH0AG14ZE
c	41	15	68.2	326	14	CD856671	CD856671 DH0AG22ZD
c	42	15	68.2	326	14	CD856685	CD856685 DH0AG22ZE
c	43	15	68.2	326	14	CD856795	CD856795 DH0AG23ZG
c	44	15	68.2	344	14	CD858273	CD858273 DH0AG14ZD
c	45	15	68.2	345	14	CD856625	CD856625 DH0AG21ZH

ALIGNMENTS

RESULT 1
AI212321/c
LOCUS AI212321 213 bp mRNA linear EST 19-OCT-1998
DEFINITION x2g02a1.f1 Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Emericella nidulans cDNA clone x2g02a1 3', mRNA sequence.
ACCESSION AI212321
VERSION AI212321.1 GI:3774263
KEYWORDS EST.
SOURCE Emericella nidulans (anamorph: Aspergillus nidulans)
ORGANISM Emericella nidulans
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Emericella.
REFERENCE 1 (bases 1 to 213)
AUTHORS Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R., Prade,R. and Roe,B.
TITLE An Aspergillus nidulans EST Database
JOURNAL Unpublished (1998)
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal Genetics Stock Center

Seq primer: M13-20
High quality sequence stop: 88.
FEATURES Location/Qualifiers
source 1. .213
/organism="Emericella nidulans"
/mol_type="mRNA"
/strain="FGSC A26"
/db_xref="taxon:162425"
/clone="x2g02a1"
/tissue_type="vegetative mycelia, asexual structures"
/clone_lib="Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library"
/note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript 3' end of cDNA cloned into XhoI site of pBluescript"
ORIGIN

Query Match 72.7%; Score 16; DB 9; Length 213;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCCGAGAACGTATTCA 22
||||||||||||||||
Db 98 CCCGAGAACGTATTCA 83

RESULT 2
BF064383/c
LOCUS BF064383 258 bp mRNA linear EST 17-OCT-2000
DEFINITION SWOvAFCAP48B11SK Onchocerca volvulus adult female cDNA (SAW98MLW-OvAF) Onchocerca volvulus cDNA clone SWOvAFCAP48B11 5', mRNA sequence.
ACCESSION BF064383
VERSION BF064383.1 GI:10841022
KEYWORDS EST.
SOURCE Onchocerca volvulus
ORGANISM Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.
REFERENCE 1 (bases 1 to 258)
AUTHORS Lizotte-Waniewski,M. and Williams,S.A.
TITLE Genes expressed in adult female stage of Onchocerca volvulus
JOURNAL Unpublished (1998)
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
FEATURES Location/Qualifiers
source 1. .258
/organism="Onchocerca volvulus"
/mol_type="mRNA"
/db_xref="taxon:6282"
/clone="SWOvAFCAP48B11"
/sex="female"
/dev_stage="adult"
/lab_host="XL1-Blue MRF'"
/clone_lib="Onchocerca volvulus adult female cDNA (SAW98MLW-OvAF)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Two adult female worms of Onchocerca volvulus were isolated from consenting patients and quick frozen. Adult female mRNA was converted.to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 7 x 10E5 independent recombinants and the average insert size is ~1100bp.The library was constructed by Michelle Lizotte-Waniewski with worms provided by Dr. Sara Lustigman. The library is available from Dr.Steven A. Williams, email: genome@smith.edu."
ORIGIN

Query Match 72.7%; Score 16; DB 10; Length 258;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCCGAGAACGTATTCA 22
||||||||||||||||
Db 102 CCCGAGAACGTATTCA 87

RESULT 3
AI585049/c
LOCUS AI585049 262 bp mRNA linear EST 07-JUN-2001
DEFINITION fb69g07.x1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone IMAGE:3717180 3', mRNA sequence.
ACCESSION AI585049
VERSION AI585049.1 GI:4570946
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 262)
AUTHORS Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE WashU Zebrafish EST Project 1998
JOURNAL Unpublished (1998)
COMMENT Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address: www.rzpd.de)
zebrafish identity (p-value greater than 1e-99) found to: gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio rerio cDNA
Seq primer: T7 ET from Amersham
High quality sequence stop: 254
POLYA=No.
FEATURES Location/Qualifiers
source 1. .262
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:3717180"
/sex="mixed"
/tissue_type="26 somite embryos, adult livers, shield stage embryos"
/lab_host="XL1-blue MRF"
/clone_lib="Zebrafish WashU MPIMG EST"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; 1st strand cDNA was primed with a Not I - oligo(dT)15 primer [5'pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTT3']; double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORT1 vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik,Berlin). cDNAs for EST

analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality control."

ORIGIN

Query Match 72.7%; Score 16; DB 9; Length 262;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          3 AAGGCCCGAGAACGTA 18
              ||||||||||||||||
Db        196 AAGGCCCGAGAACGTA 181
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RESULT 4
AI211182/c
LOCUS AI211182 285 bp mRNA linear EST 19-OCT-1998
DEFINITION o0c05a1.f1 Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Emericella nidulans cDNA clone o0c05a1 3', mRNA sequence.
ACCESSION AI211182
VERSION AI211182.1 GI:3773124
KEYWORDS EST.
SOURCE Emericella nidulans (anamorph: Aspergillus nidulans)
ORGANISM Emericella nidulans
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Emericella.
REFERENCE 1 (bases 1 to 285)
AUTHORS Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R., Prade,R. and Roe,B.
TITLE An Aspergillus nidulans EST Database
JOURNAL Unpublished (1998)
COMMENT Other_ESTs: o0c05a1.r1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal Genetics Stock Center
Seq primer: M13-20
High quality sequence stop: 219.
FEATURES Location/Qualifiers
source 1. .285
/organism="Emericella nidulans"
/mol_type="mRNA"
/strain="FGSC A26"
/db_xref="taxon:162425"
/clone="o0c05a1"
/tissue_type="vegetative mycelia, asexual structures"
/clone_lib="Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library"
/note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript 3' end of cDNA cloned into XhoI site of pBluescript"
ORIGIN

Query Match 72.7%; Score 16; DB 9; Length 285;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          7 CCCGAGAACGTATTCA 22
              ||||||||||||||||
Db         92 CCCGAGAACGTATTCA 77
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RESULT 5
AI381122/c
LOCUS AI381122 324 bp mRNA linear EST 26-JAN-1999
DEFINITION SWOvAFCAP30F01SK Onchocerca volvulus adult female cDNA (SAW98MLW-OvAF) Onchocerca volvulus cDNA clone SWOvAFCAP30F01 5', mRNA sequence.
ACCESSION AI381122
VERSION AI381122.1 GI:4191665
KEYWORDS EST.
SOURCE Onchocerca volvulus
ORGANISM Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.
REFERENCE 1 (bases 1 to 324)
AUTHORS Lizotte-Waniewski,M. and Williams,S.A.
TITLE Genes expressed in adult female stage of Onchocerca volvulus
JOURNAL Unpublished (1998)
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
FEATURES Location/Qualifiers
source 1. .324
/organism="Onchocerca volvulus"
/mol_type="mRNA"
/db_xref="taxon:6282"
/clone="SWOvAFCAP30F01"
/sex="female"
/dev_stage="adult"
/lab_host="XL1-Blue MRF'"
/clone_lib="Onchocerca volvulus adult female cDNA (SAW98MLW-OvAF)"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Two adult female worms of Onchocerca volvulus were isolated from consenting patients and quick frozen. Adult female mRNA was converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 7 x 10E5 independent recombinants and the average insert size is ~1100bp.The library was constructed by Michelle Lizotte-Waniewski with worms provided by Dr. Sara Lustigman. The library is available from Dr.Steven A. Williams, email: genome@smith.edu."
ORIGIN

Query Match 72.7%; Score 16; DB 9; Length 324;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          7 CCCGAGAACGTATTCA 22
              ||||||||||||||||
Db        192 CCCGAGAACGTATTCA 177
```

RESULT 6
AA497171/c
LOCUS AA497171 348 bp mRNA linear EST 30-JUN-1997
DEFINITION fa01g09.s1 Zebrafish ICRFzfls Danio rerio cDNA clone 3D9 3', mRNA sequence.
ACCESSION AA497171
VERSION AA497171.1 GI:2230492
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

```
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Clark,M., Lehrach,H., Appel,B., Eisen,J., Johnson,S., Marra,M.,
            Eddy,S., Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G.,
            Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Martin,J., Moore,B.,
            Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y.,
            Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Steve Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Steve Johnson lab internal ID - P1_89 NOTE - For this library, the
            CLONE id field represents a position identifier on the original
            cDNA library preparation plate. cDNA Library Preparation: Matthew
            Clark: cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by:
            Washington University Genome Sequencing Center Clone distribution:
            Genome Systems, St. Louis, and Max Planck Institut fuer Molekulare
            Genetik, Berlin Tel +49 30 84 13 1235
            Seq primer: -40m13 ET from Amersham
            High quality sequence stop: 315.
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="3D9"
                     /sex="mixed"
                     /tissue_type="pooled 26-somite embryos"
                     /lab_host="XL1-blue MRF"
                     /clone_lib="Zebrafish ICRFzfls"
                     /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; 1st
                     strand cDNA was primed with a Not I - oligo(dT)15 primer
                     [5'pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT3'], on
                     mRNA from pooled 26 somite zebrafish embryos;
                     double-stranded cDNA was ligated to Sal I adaptors (BRL),
                     digested with Not I and cloned into the Not I and Sal I
                     sites of the pSPORT1 vector (BRL). Library was constructed
                     by Matthew Clark (Lehrach lab; ICRF, London and  Max
                     Planck Institut fuer Molekulare Genetik, Berlin) and was
                     not biochemically normalised.  70,000 clones from this
                     library were arrayed on high density filters and
                     subsequently screened by oligonucleotide hybridization
                     fingerprinting to identify unique or minimally redundant
                     clones for more intensive analysis."
ORIGIN

  Query Match             72.7%;  Score 16;  DB 9;  Length 348;
  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 AAGGCCCGAGAACGTA 18
              ||||||||||||||||
Db        196 AAGGCCCGAGAACGTA 181


RESULT 7
BI897005
LOCUS       BI897005                367 bp    mRNA    linear   EST 15-OCT-2001
DEFINITION  fk52e10.y1 Zebrafish 15-19hr embryonic cDNA Danio rerio cDNA 5',
            mRNA sequence.
ACCESSION   BI897005
VERSION     BI897005.1  GI:16140141
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 367)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Other_ESTs: fk52e10.x1
            Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            Library constructed by: Bernhard Korn DNA Sequencing by: Washington
            University Genome Sequencing Center Clone distribution:
            RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
            www.rzpd.de)
            zebrafish identity (p-value greater than 1e-99) found to:
            gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio
            rerio cDNA
            Seq primer: T3 ET from Amersham
            High quality sequence stop: 320.
FEATURES             Location/Qualifiers
     source          1. .367
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /strain="unspecified"
                     /db_xref="taxon:7955"
                     /sex="mixed"
                     /dev_stage="15-19 hour embryo"
                     /lab_host="E.Coli (DH10B/XL2blue)"
                     /clone_lib="Zebrafish 15-19hr embryonic cDNA"
                     /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; This
                     Zebrafish library was constructed by Dr. Bernhard Korn
                     (email: b.korn@dkfz-heidelberg.de). RZPD library number:
                     717"
ORIGIN

  Query Match             72.7%;  Score 16;  DB 12;  Length 367;
  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 AAGGCCCGAGAACGTA 18
              ||||||||||||||||
Db        250 AAGGCCCGAGAACGTA 265


RESULT 8
BI897004/c
LOCUS       BI897004                371 bp    mRNA    linear   EST 15-OCT-2001
DEFINITION  fk52e10.x1 Zebrafish 15-19hr embryonic cDNA Danio rerio cDNA 3',
            mRNA sequence.
ACCESSION   BI897004
VERSION     BI897004.1  GI:16140140
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 371)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
```

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
Library constructed by: Bernhard Korn DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address: www.rzpd.de)
zebrafish identity (p-value greater than 1e-99) found to: gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio rerio cDNA
Seq primer: T7 from Gibco.

FEATURES Location/Qualifiers
source 1. .371
/organism="Danio rerio"
/mol_type="mRNA"
/strain="unspecified"
/db_xref="taxon:7955"
/sex="mixed"
/dev_stage="15-19 hour embryo"
/lab_host="E.Coli (DH10B/XL2blue)"
/clone_lib="Zebrafish 15-19hr embryonic cDNA"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; This Zebrafish library was constructed by Dr. Bernhard Korn (email: b.korn@dkfz-heidelberg.de). RZPD library number: 717"

ORIGIN

Query Match 72.7%; Score 16; DB 12; Length 371;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AAGGCCCGAGAACGTA 18
||||||||||||||||
Db 168 AAGGCCCGAGAACGTA 153

RESULT 9
AA784579/c
LOCUS AA784579 377 bp mRNA linear EST 29-JUL-1998
DEFINITION f1h09a1.f1 Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Emericella nidulans cDNA clone f1h09a1 3', mRNA sequence.
ACCESSION AA784579
VERSION AA784579.1 GI:2844747
KEYWORDS EST.
SOURCE Emericella nidulans (anamorph: Aspergillus nidulans)
ORGANISM Emericella nidulans
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Emericella.
REFERENCE 1 (bases 1 to 377)
AUTHORS Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R., Prade,R. and Roe,B.
TITLE An Aspergillus nidulans EST Database
JOURNAL Unpublished (1998)
COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal Genetics Stock Center
Seq primer: M13-20
High quality sequence stop: 324.

FEATURES Location/Qualifiers
source 1. .377
/organism="Emericella nidulans"
/mol_type="mRNA"
/strain="FGSC A26"
/db_xref="taxon:162425"
/clone="f1h09a1"
/tissue_type="vegetative mycelia, asexual structures"
/clone_lib="Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library"
/note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript 3' end of cDNA cloned into XhoI site of pBluescript"

ORIGIN

Query Match 72.7%; Score 16; DB 9; Length 377;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCCGAGAACGTATTCA 22
||||||||||||||||
Db 134 CCCGAGAACGTATTCA 119

RESULT 10
BI896339/c
LOCUS BI896339 445 bp mRNA linear EST 15-OCT-2001
DEFINITION fc43d02.x1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone IMAGE:3724131 3', mRNA sequence.
ACCESSION BI896339
VERSION BI896339.1 GI:16139475
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 445)
AUTHORS Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE WashU Zebrafish EST Project 1998
JOURNAL Unpublished (1998)
COMMENT Other_ESTs: fc43d02.y1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address: www.rzpd.de)
zebrafish identity (p-value greater than 1e-99) found to: gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio rerio cDNA
Seq primer: T7 from Gibco
High quality sequence stop: 435.

FEATURES Location/Qualifiers
source 1. .445
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:3724131"
/sex="mixed"
/tissue_type="26 somite embryos, adult livers, shield stage embryos"
/lab_host="XL1-blue MRF"
/clone_lib="Zebrafish WashU MPIMG EST"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; 1st strand cDNA was primed with a Not I - oligo(dT)15 primer [5'pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT3'];

double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORT1 vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik,Berlin). cDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality control."

ORIGIN

Query Match 72.7%; Score 16; DB 12; Length 445;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 AAGGCCCGAGAACGTA 18
              ||||||||||||||||
Db        189 AAGGCCCGAGAACGTA 174
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RESULT 11
BM156391/c
LOCUS BM156391 445 bp mRNA linear EST 26-JUL-2002
DEFINITION fv18f06.y2 zebrafish adult brain Danio rerio cDNA clone IMAGE:5386907 5', mRNA sequence.
ACCESSION BM156391
VERSION BM156391.1 GI:17240087
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 445)
AUTHORS Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE WashU Zebrafish EST Project 1998
JOURNAL Unpublished (1998)
COMMENT Other_ESTs: fv18f06.x2
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: John Ngai. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address: www.rzpd.de)
Putative full length read
The vector to vector length is 522
Seq primer: T7.
FEATURES Location/Qualifiers
source 1. .445
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:5386907"
/sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
/lab_host="E. coli DH10B"
/clone_lib="zebrafish adult brain"
/note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI; Original library was constructed in lambdaZIPLOX. Mass excision of the cDNA library was performed to yield pZIPLOX plasmids. Insert check was done in original library."

ORIGIN

Query Match 72.7%; Score 16; DB 12; Length 445;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 AAGGCCCGAGAACGTA 18
              ||||||||||||||||
Db         16 AAGGCCCGAGAACGTA 1
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RESULT 12
BI533213/c
LOCUS BI533213 448 bp mRNA linear EST 26-JUL-2002
DEFINITION fr79a06.x1 zebrafish adult brain Danio rerio cDNA clone IMAGE:4966930 3', mRNA sequence.
ACCESSION BI533213
VERSION BI533213.1 GI:15373780
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 448)
AUTHORS Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE WashU Zebrafish EST Project 1998
JOURNAL Unpublished (1998)
COMMENT Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: John Ngai. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address: www.rzpd.de)
zebrafish identity (p-value greater than 1e-99) found to: gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio rerio cDNA
Seq primer: -40UP
High quality sequence stop: 408.
FEATURES Location/Qualifiers
source 1. .448
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:4966930"
/sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
/lab_host="E. coli DH10B"
/clone_lib="zebrafish adult brain"
/note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI;

Original library was constructed in lambdaZIPLOX. Mass excision of the cDNA library was performed to yield pZIPLOX plasmids. Insert check was done in original library."

ORIGIN

Query Match 72.7%; Score 16; DB 12; Length 448;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          3 AAGGCCCGAGAACGTA 18
              ||||||||||||||||
Db        181 AAGGCCCGAGAACGTA 166
```

RESULT 13
BM102203/c
LOCUS BM102203 452 bp mRNA linear EST 26-JUL-2002
DEFINITION fv14d10.x1 zebrafish adult brain Danio rerio cDNA clone IMAGE:5386435 3', mRNA sequence.
ACCESSION BM102203
VERSION BM102203.1 GI:17033271
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 452)
AUTHORS Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE WashU Zebrafish EST Project 1998
JOURNAL Unpublished (1998)
COMMENT Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: John Ngai. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address: www.rzpd.de)
zebrafish identity (p-value greater than 1e-99) found to: gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio rerio cDNA
Seq primer: -40UP
High quality sequence stop: 451.

FEATURES Location/Qualifiers
source 1. .452
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:5386435"
/sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
/lab_host="E. coli DH10B"
/clone_lib="zebrafish adult brain"
/note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI; Original library was constructed in lambdaZIPLOX. Mass excision of the cDNA library was performed to yield pZIPLOX plasmids. Insert check was done in original library."

ORIGIN

Query Match 72.7%; Score 16; DB 12; Length 452;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          3 AAGGCCCGAGAACGTA 18
              ||||||||||||||||
Db        180 AAGGCCCGAGAACGTA 165
```

RESULT 14
BI896999/c
LOCUS BI896999 458 bp mRNA linear EST 15-OCT-2001
DEFINITION fk50e03.x1 Zebrafish 15-19hr embryonic cDNA Danio rerio cDNA 3', mRNA sequence.
ACCESSION BI896999
VERSION BI896999.1 GI:16140135
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 458)
AUTHORS Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE WashU Zebrafish EST Project 1998
JOURNAL Unpublished (1998)
COMMENT Other_ESTs: fk50e03.y1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
Library constructed by: Bernhard Korn DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address: www.rzpd.de)
zebrafish identity (p-value greater than 1e-99) found to: gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio rerio cDNA
Seq primer: T7 from Gibco
High quality sequence stop: 434.

FEATURES Location/Qualifiers
source 1. .458
/organism="Danio rerio"
/mol_type="mRNA"
/strain="unspecified"
/db_xref="taxon:7955"
/sex="mixed"
/dev_stage="15-19 hour embryo"
/lab_host="E.Coli (DH10B/XL2blue)"
/clone_lib="Zebrafish 15-19hr embryonic cDNA"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; This Zebrafish library was constructed by Dr. Bernhard Korn (email: b.korn@dkfz-heidelberg.de). RZPD library number: 717"

ORIGIN

Query Match 72.7%; Score 16; DB 12; Length 458;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 AAGGCCCGAGAACGTA 18
              ||||||||||||||||
Db         93 AAGGCCCGAGAACGTA 78
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RESULT 15
BI708149/c
LOCUS BI708149 459 bp mRNA linear EST 19-SEP-2001
DEFINITION fs42g04.x1 Zebrafish adult olfactory Danio rerio cDNA clone IMAGE:5070534 3', mRNA sequence.
ACCESSION BI708149
VERSION BI708149.1 GI:15683844
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 459)
AUTHORS Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE WashU Zebrafish EST Project 1998
JOURNAL Unpublished (1998)
COMMENT Other_ESTs: fs42g04.y1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: John Ngai cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address: www.rzpd.de)
zebrafish identity (p-value greater than 1e-99) found to: gi|2230492|gb|AA497171|AA497171 fa01g09.s1 Zebrafish ICRFzfls Danio rerio cDNA
Seq primer: T7 from Gibco
High quality sequence stop: 440.
FEATURES Location/Qualifiers
source 1. .459
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:5070534"
/sex="mixed"
/tissue_type="Olfactory rosettes"
/dev_stage="adult"
/lab_host="D10Hb (Gibco BRL)"
/clone_lib="Zebrafish adult olfactory"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; This is a directionally cloned cDNA library from adult Zebrafish olfactory epithelium."
ORIGIN

Query Match 72.7%; Score 16; DB 12; Length 459;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 AAGGCCCGAGAACGTA 18
              ||||||||||||||||
Db        167 AAGGCCCGAGAACGTA 152
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Search completed: August 4, 2004, 09:20:54
Job time : 1535.58 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 04:00:30 ; Search time 164.337 Seconds
(without alignments)
517.009 Million cell updates/sec

Title: US-09-940-860-2
Perfect score: 20
Sequence: 1 ggaggaaggcgaggatgacg 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	1172	3	AAA37798	Aaa37798 Helicobac
	2	20	100.0	1194	3	AAA37797	Aaa37797 Helicobac
	3	20	100.0	1236	3	AAA37796	Aaa37796 Helicobac
	4	20	100.0	1267	3	AAA37795	Aaa37795 Helicobac
	5	20	100.0	1299	3	AAA37794	Aaa37794 Helicobac
	6	20	100.0	1331	3	AAA37793	Aaa37793 Helicobac
	7	20	100.0	1335	3	AAA37791	Aaa37791 Helicobac
	8	20	100.0	1548	2	AAV66849	Aav66849 Chlamydia
	9	20	100.0	1548	2	AAV66846	Aav66846 Chlamydia
	10	20	100.0	1548	2	AAV66848	Aav66848 Chlamydia
	11	20	100.0	1548	2	AAV66845	Aav66845 Chlamydia
	12	20	100.0	1548	2	AAV66850	Aav66850 Chlamydia
	13	20	100.0	1548	2	AAV66847	Aav66847 Chlamydia
	14	20	100.0	1548	5	AAS11031	Aas11031 Chlamydia
	15	20	100.0	1549	2	AAV66851	Aav66851 Chlamydia
	16	20	100.0	2751	4	AAH28376	Aah28376 Intergeni
	17	20	100.0	2762	4	AAH28407	Aah28407 Intergeni
c	18	20	100.0	110000	2	AAZ01425_06	Continuation (7 of
	19	20	100.0	110000	2	AAX91990_10	Continuation (11 o
	20	17	85.0	1073	7	ABZ34685	Abz34685 Coding se
	21	16	80.0	1251	7	ACA30087	Aca30087 Prokaryot
	22	16	80.0	3264	7	ADA69779	Ada69779 Rice gene
	23	16	80.0	5536	4	AAS46575	Aas46575 Tumour su
	24	16	80.0	5536	6	ABL33832	Abl33832 Human imm
	25	15	75.0	278	6	ABQ78796	Abq78796 Nucleotid
c	26	15	75.0	281	6	ABL71499	Abl71499 Corn tass
c	27	15	75.0	294	6	ABL76470	Abl76470 Corn tass
	28	15	75.0	308	6	ABQ78794	Abq78794 Nucleotid
	29	15	75.0	348	4	AAL25889	Aal25889 Human bre
	30	15	75.0	351	6	ABQ78795	Abq78795 Nucleotid
c	31	15	75.0	357	6	ABQ85719	Abq85719 Arabidops
	32	15	75.0	358	4	AAL19054	Aal19054 Human bre
	33	15	75.0	358	4	AAL08144	Aal08144 Human bre
	34	15	75.0	384	5	AAS79337	Aas79337 DNA encod
c	35	15	75.0	390	5	AAF67474	Aaf67474 Novel hum
	36	15	75.0	400	5	AAF67301	Aaf67301 Novel hum
	37	15	75.0	405	5	ABV13787	Abv13787 Human pro
	38	15	75.0	405	6	ABL81917	Abl81917 Human ova
	39	15	75.0	417	2	AAV89330	Aav89330 EST clone
	40	15	75.0	443	5	ABV34900	Abv34900 Human pro
	41	15	75.0	443	5	ABV43749	Abv43749 Human pro
c	42	15	75.0	494	9	ADC76303	Adc76303 DNA homol
c	43	15	75.0	494	9	ADC76983	Adc76983 DNA homol
	44	15	75.0	525	6	ABZ14572	Abz14572 Arabidops
	45	15	75.0	746	3	AAC48695	Aac48695 Arabidops

ALIGNMENTS

RESULT 1
AAA37798
ID AAA37798 standard; DNA; 1172 BP.
XX
AC AAA37798;
XX
DT 15-SEP-2003 (revised)
DT 15-JAN-2001 (first entry)
XX
DE Helicobacter 16SrRna DNA sequence R28TOTAAL.
XX
KW Helicobacter; 16SrRNA; detection; strain identification; gastric ulcer;
KW chronic gastritis; zoonoses; ss.
XX
OS Candidatus Helicobacter bovis.
XX
PN EP1035219-A1.
XX
PD 13-SEP-2000.
XX
PF 25-FEB-1999; 99EP-00870035.
XX
PR 25-FEB-1999; 99EP-00870035.
XX
PA (UYGE-) UNIV GENT.
XX
PI Ducatelle R, De Groote D, Haesebrouck F, Quint W, Van Doorn L;
XX
DR WPI; 2000-559879/52.
XX
PT Novel isolated 16S rDNA Helicobacter polynucleotides useful as probes or
PT primers for detecting and/or typing Helicobacter strains present in a
PT biological sample.
XX
PS Claim 2; Page 24-25; 132pp; English.
XX
CC This sequence represents a Helicobacter 16SrRNA sequence of the
CC invention. A probe which specifically hybridises to the 16SrRNA sequence
CC and a primer which specifically amplifies it are used for detecting
CC and/or typing Helicobacter strains present in a biological sample
CC (obtained from mammals preferably cattle and pigs) by hybridising or
CC specifically amplifying the 16S rRNA gene target region of Helicobacter
CC strains present in the biological sample with the primer or probe,
CC respectively. The 16S rRNA sequence is also used as a medicament. The 16S
CC rRNA sequences are used for studying and detecting pathogenic
CC Helicobacter strains which cause gastric ulcers and chronic gastritis in

```
CC   mammals, particularly cattle and pigs. The method is also useful for
CC   detection of zoonoses in humans. (Updated on 15-SEP-2003 to standardise
CC   OS field)
XX
SQ   Sequence 1172 BP; 323 A; 259 C; 345 G; 245 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 20;  DB 3;  Length 1172;
  Best Local Similarity  100.0%;  Pred. No. 0.34;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
              ||||||||||||||||||||
Db       1016 GGAGGAAGGCGAGGATGACG 1035


RESULT 2
AAA37797
ID   AAA37797 standard; DNA; 1194 BP.
XX
AC   AAA37797;
XX
DT   15-SEP-2003  (revised)
DT   15-JAN-2001  (first entry)
XX
DE   Helicobacter 16SrRna DNA sequence R27TOTAAL.
XX
KW   Helicobacter; 16SrRNA; detection; strain identification; gastric ulcer;
KW   chronic gastritis; zoonoses; ss.
XX
OS   Candidatus Helicobacter bovis.
XX
PN   EP1035219-A1.
XX
PD   13-SEP-2000.
XX
PF   25-FEB-1999;   99EP-00870035.
XX
PR   25-FEB-1999;   99EP-00870035.
XX
PA   (UYGE-) UNIV GENT.
XX
PI   Ducatelle R,  De Groote D,  Haesebrouck F,  Quint W,  Van Doorn L;
XX
DR   WPI; 2000-559879/52.
XX
PT   Novel isolated 16S rDNA Helicobacter polynucleotides useful as probes or
PT   primers for detecting and/or typing Helicobacter strains present in a
PT   biological sample.
XX
PS   Claim 2; Page 24; 132pp; English.
XX
CC   This sequence represents a Helicobacter 16SrRNA sequence of the
CC   invention. A probe which specifically hybridises to the 16SrRNA sequence
CC   and a primer which specifically amplifies it are used for detecting
CC   and/or typing Helicobacter strains present in a biological sample
CC   (obtained from mammals preferably cattle and pigs) by hybridising or
CC   specifically amplifying the 16S rRNA gene target region of Helicobacter
CC   strains present in the biological sample with the primer or probe,
CC   respectively. The 16S rRNA sequence is also used as a medicament. The 16S
CC   rRNA sequences are used for studying and detecting pathogenic
CC   Helicobacter strains which cause gastric ulcers and chronic gastritis in
CC   mammals, particularly cattle and pigs. The method is also useful for
CC   detection of zoonoses in humans. (Updated on 15-SEP-2003 to standardise
CC   OS field)
XX
SQ   Sequence 1194 BP; 327 A; 263 C; 356 G; 248 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 20;  DB 3;  Length 1194;
  Best Local Similarity  100.0%;  Pred. No. 0.34;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
              ||||||||||||||||||||
Db       1035 GGAGGAAGGCGAGGATGACG 1054


RESULT 3
AAA37796
ID   AAA37796 standard; DNA; 1236 BP.
XX
AC   AAA37796;
XX
DT   15-SEP-2003  (revised)
DT   15-JAN-2001  (first entry)
XX
DE   Helicobacter 16SrRna DNA sequence R13D001INV.
XX
KW   Helicobacter; 16SrRNA; detection; strain identification; gastric ulcer;
KW   chronic gastritis; zoonoses; ss.
XX
OS   Candidatus Helicobacter bovis.
XX
PN   EP1035219-A1.
XX
PD   13-SEP-2000.
XX
PF   25-FEB-1999;   99EP-00870035.
XX
PR   25-FEB-1999;   99EP-00870035.
XX
PA   (UYGE-) UNIV GENT.
XX
PI   Ducatelle R,  De Groote D,  Haesebrouck F,  Quint W,  Van Doorn L;
XX
DR   WPI; 2000-559879/52.
XX
PT   Novel isolated 16S rDNA Helicobacter polynucleotides useful as probes or
PT   primers for detecting and/or typing Helicobacter strains present in a
PT   biological sample.
XX
PS   Claim 2; Page 23-24; 132pp; English.
XX
CC   This sequence represents a Helicobacter 16SrRNA sequence of the
CC   invention. A probe which specifically hybridises to the 16SrRNA sequence
CC   and a primer which specifically amplifies it are used for detecting
CC   and/or typing Helicobacter strains present in a biological sample
CC   (obtained from mammals preferably cattle and pigs) by hybridising or
CC   specifically amplifying the 16S rRNA gene target region of Helicobacter
CC   strains present in the biological sample with the primer or probe,
CC   respectively. The 16S rRNA sequence is also used as a medicament. The 16S
CC   rRNA sequences are used for studying and detecting pathogenic
CC   Helicobacter strains which cause gastric ulcers and chronic gastritis in
CC   mammals, particularly cattle and pigs. The method is also useful for
CC   detection of zoonoses in humans. (Updated on 15-SEP-2003 to standardise
CC   OS field)
XX
SQ   Sequence 1236 BP; 336 A; 271 C; 369 G; 259 T; 0 U; 1 Other;

  Query Match            100.0%;  Score 20;  DB 3;  Length 1236;
  Best Local Similarity  100.0%;  Pred. No. 0.34;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
              ||||||||||||||||||||
Db       1058 GGAGGAAGGCGAGGATGACG 1077


RESULT 4
AAA37795
ID   AAA37795 standard; DNA; 1267 BP.
XX
AC   AAA37795;
XX
DT   15-SEP-2003  (revised)
DT   15-JAN-2001  (first entry)
XX
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DE Helicobacter 16SrRna DNA sequence R6XA001.
XX
KW Helicobacter; 16SrRNA; detection; strain identification; gastric ulcer;
KW chronic gastritis; zoonoses; ss.
XX
OS Candidatus Helicobacter bovis.
XX
PN EP1035219-A1.
XX
PD 13-SEP-2000.
XX
PF 25-FEB-1999; 99EP-00870035.
XX
PR 25-FEB-1999; 99EP-00870035.
XX
PA (UYGE-) UNIV GENT.
XX
PI Ducatelle R, De Groote D, Haesebrouck F, Quint W, Van Doorn L;
XX
DR WPI; 2000-559879/52.
XX
PT Novel isolated 16S rDNA Helicobacter polynucleotides useful as probes or
PT primers for detecting and/or typing Helicobacter strains present in a
PT biological sample.
XX
PS Claim 2; Page 23; 132pp; English.
XX
CC This sequence represents a Helicobacter 16SrRNA sequence of the
CC invention. A probe which specifically hybridises to the 16SrRNA sequence
CC and a primer which specifically amplifies it are used for detecting
CC and/or typing Helicobacter strains present in a biological sample
CC (obtained from mammals preferably cattle and pigs) by hybridising or
CC specifically amplifying the 16S rRNA gene target region of Helicobacter
CC strains present in the biological sample with the primer or probe,
CC respectively. The 16S rRNA sequence is also used as a medicament. The 16S
CC rRNA sequences are used for studying and detecting pathogenic
CC Helicobacter strains which cause gastric ulcers and chronic gastritis in
CC mammals, particularly cattle and pigs. The method is also useful for
CC detection of zoonoses in humans. (Updated on 15-SEP-2003 to standardise
CC OS field)
XX
SQ Sequence 1267 BP; 350 A; 272 C; 375 G; 270 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 1267;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAAGGCGAGGATGACG 20
||||||||||||||||||||
Db 1072 GGAGGAAGGCGAGGATGACG 1091

RESULT 5
AAA37794
ID AAA37794 standard; DNA; 1299 BP.
XX
AC AAA37794;
XX
DT 15-SEP-2003 (revised)
DT 15-JAN-2001 (first entry)
XX
DE Helicobacter 16SrRna DNA sequence R3XA001.
XX
KW Helicobacter; 16SrRNA; detection; strain identification; gastric ulcer;
KW chronic gastritis; zoonoses; ss.
XX
OS Candidatus Helicobacter bovis.
XX
PN EP1035219-A1.
XX
PD 13-SEP-2000.
XX
PF 25-FEB-1999; 99EP-00870035.
XX
PR 25-FEB-1999; 99EP-00870035.
XX
PA (UYGE-) UNIV GENT.
XX
PI Ducatelle R, De Groote D, Haesebrouck F, Quint W, Van Doorn L;
XX
DR WPI; 2000-559879/52.
XX
PT Novel isolated 16S rDNA Helicobacter polynucleotides useful as probes or
PT primers for detecting and/or typing Helicobacter strains present in a
PT biological sample.
XX
PS Claim 2; Page 22-23; 132pp; English.
XX
CC This sequence represents a Helicobacter 16SrRNA sequence of the
CC invention. A probe which specifically hybridises to the 16SrRNA sequence
CC and a primer which specifically amplifies it are used for detecting
CC and/or typing Helicobacter strains present in a biological sample
CC (obtained from mammals preferably cattle and pigs) by hybridising or
CC specifically amplifying the 16S rRNA gene target region of Helicobacter
CC strains present in the biological sample with the primer or probe,
CC respectively. The 16S rRNA sequence is also used as a medicament. The 16S
CC rRNA sequences are used for studying and detecting pathogenic
CC Helicobacter strains which cause gastric ulcers and chronic gastritis in
CC mammals, particularly cattle and pigs. The method is also useful for
CC detection of zoonoses in humans. (Updated on 15-SEP-2003 to standardise
CC OS field)
XX
SQ Sequence 1299 BP; 357 A; 283 C; 385 G; 274 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 1299;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAAGGCGAGGATGACG 20
||||||||||||||||||||
Db 1103 GGAGGAAGGCGAGGATGACG 1122

RESULT 6
AAA37793
ID AAA37793 standard; DNA; 1331 BP.
XX
AC AAA37793;
XX
DT 15-SEP-2003 (revised)
DT 15-JAN-2001 (first entry)
XX
DE Helicobacter 16SrRna DNA sequence R5XE001.
XX
KW Helicobacter; 16SrRNA; detection; strain identification; gastric ulcer;
KW chronic gastritis; zoonoses; ss.
XX
OS Candidatus Helicobacter bovis.
XX
PN EP1035219-A1.
XX
PD 13-SEP-2000.
XX
PF 25-FEB-1999; 99EP-00870035.
XX
PR 25-FEB-1999; 99EP-00870035.
XX
PA (UYGE-) UNIV GENT.
XX
PI Ducatelle R, De Groote D, Haesebrouck F, Quint W, Van Doorn L;
XX
DR WPI; 2000-559879/52.
XX
PT Novel isolated 16S rDNA Helicobacter polynucleotides useful as probes or
PT primers for detecting and/or typing Helicobacter strains present in a
PT biological sample.

XX
PS Claim 2; Page 22; 132pp; English.
XX
CC This sequence represents a Helicobacter 16SrRNA sequence of the
CC invention. A probe which specifically hybridises to the 16SrRNA sequence
CC and a primer which specifically amplifies it are used for detecting
CC and/or typing Helicobacter strains present in a biological sample
CC (obtained from mammals preferably cattle and pigs) by hybridising or
CC specifically amplifying the 16S rRNA gene target region of Helicobacter
CC strains present in the biological sample with the primer or probe,
CC respectively. The 16S rRNA sequence is also used as a medicament. The 16S
CC rRNA sequences are used for studying and detecting pathogenic
CC Helicobacter strains which cause gastric ulcers and chronic gastritis in
CC mammals, particularly cattle and pigs. The method is also useful for
CC detection of zoonoses in humans. (Updated on 15-SEP-2003 to standardise
CC OS field)
XX
SQ Sequence 1331 BP; 366 A; 292 C; 389 G; 284 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 1331;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAAGGCGAGGATGACG 20
||||||||||||||||||||
Db 1103 GGAGGAAGGCGAGGATGACG 1122

RESULT 7
AAA37791
ID AAA37791 standard; DNA; 1335 BP.
XX
AC AAA37791;
XX
DT 15-SEP-2003 (revised)
DT 15-JAN-2001 (first entry)
XX
DE Helicobacter 16SrRna DNA sequence R2XA001.
XX
KW Helicobacter; 16SrRNA; detection; strain identification; gastric ulcer;
KW chronic gastritis; zoonoses; ss.
XX
OS Candidatus Helicobacter bovis.
XX
PN EP1035219-A1.
XX
PD 13-SEP-2000.
XX
PF 25-FEB-1999; 99EP-00870035.
XX
PR 25-FEB-1999; 99EP-00870035.
XX
PA (UYGE-) UNIV GENT.
XX
PI Ducatelle R, De Groote D, Haesebrouck F, Quint W, Van Doorn L;
XX
DR WPI; 2000-559879/52.
XX
PT Novel isolated 16S rDNA Helicobacter polynucleotides useful as probes or
PT primers for detecting and/or typing Helicobacter strains present in a
PT biological sample.
XX
PS Claim 1; Page 19; 132pp; English.
XX
CC This sequence represents a Helicobacter 16SrRNA sequence of the
CC invention. A probe which specifically hybridises to the 16SrRNA sequence
CC and a primer which specifically amplifies it are used for detecting
CC and/or typing Helicobacter strains present in a biological sample
CC (obtained from mammals preferably cattle and pigs) by hybridising or
CC specifically amplifying the 16S rRNA gene target region of Helicobacter
CC strains present in the biological sample with the primer or probe,
CC respectively. The 16S rRNA sequence is also used as a medicament. The 16S
CC rRNA sequences are used for studying and detecting pathogenic
CC Helicobacter strains which cause gastric ulcers and chronic gastritis in
CC mammals, particularly cattle and pigs. The method is also useful for
CC detection of zoonoses in humans. (Updated on 15-SEP-2003 to standardise
CC OS field)
XX
SQ Sequence 1335 BP; 364 A; 294 C; 393 G; 284 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 1335;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAAGGCGAGGATGACG 20
||||||||||||||||||||
Db 1103 GGAGGAAGGCGAGGATGACG 1122

RESULT 8
AAV66849
ID AAV66849 standard; DNA; 1548 BP.
XX
AC AAV66849;
XX
DT 17-OCT-2003 (revised)
DT 06-JAN-1999 (first entry)
XX
DE Chlamydia 16S ribosome RNA gene #5.
XX
KW Chlamydia genus; microbe; bird-hosted; 16S ribosome RNA; detection; ds.
XX
OS Chlamydophila pecorum.
XX
PN JP10262679-A.
XX
PD 06-OCT-1998.
XX
PF 28-MAR-1997; 97JP-00078591.
XX
PR 28-MAR-1997; 97JP-00078591.
XX
PA (ATAT-) A & T KK.
PA (TOKU) TOKUYAMA SODA KK.
XX
DR WPI; 1998-587294/50.
XX
PT Chlamydia species ribosome genes, and primers derived from it - used for
PT the nucleic acid amplification detection of Chlamydia species.
XX
PS Claim 1; Page 15; 18pp; Japanese.
XX
CC The present sequence represents a gene coding Chlamydia 16s ribosome RNA
CC from Chlamydia pecorum. Also described in the present invention are: (1)
CC a recombinant vector containing the above gene; and (2) a transformant
CC transformed by the above recombinant vector. The nucleic acid, and
CC primers which can hybridise to it, are used for the specific nucleic acid
CC amplification detection of a Chlamydia genus microbe i.e. detection of
CC PCR products. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 1548 BP; 402 A; 318 C; 460 G; 368 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 1548;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAAGGCGAGGATGACG 20
||||||||||||||||||||
Db 1176 GGAGGAAGGCGAGGATGACG 1195

RESULT 9
AAV66846
ID AAV66846 standard; DNA; 1548 BP.
XX
AC AAV66846;

XX
DT 17-OCT-2003 (revised)
DT 06-JAN-1999 (first entry)
XX
DE Chlamydia 16S ribosome RNA gene #2.
XX
KW Chlamydia genus; microbe; bird-hosted; 16S ribosome RNA; detection; ds.
XX
OS Chlamydophila caviae.
XX
PN JP10262679-A.
XX
PD 06-OCT-1998.
XX
PF 28-MAR-1997; 97JP-00078591.
XX
PR 28-MAR-1997; 97JP-00078591.
XX
PA (ATAT-) A & T KK.
PA (TOKU) TOKUYAMA SODA KK.
XX
DR WPI; 1998-587294/50.
XX
PT Chlamydia species ribosome genes, and primers derived from it - used for
PT the nucleic acid amplification detection of Chlamydia species.
XX
PS Claim 1; Page 13-14; 18pp; Japanese.
XX
CC The present sequence represents a gene coding Chlamydia 16s ribosome RNA
CC from Chlamydia psittaci. Also described in the present invention are: (1)
CC a recombinant vector containing the above gene; and (2) a transformant
CC transformed by the above recombinant vector. The nucleic acid, and
CC primers which can hybridise to it, are used for the specific nucleic acid
CC amplification detection of a Chlamydia genus microbe i.e. detection of
CC PCR products. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 1548 BP; 413 A; 325 C; 451 G; 359 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 1548;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAAGGCGAGGATGACG 20
||||||||||||||||||||
Db 1178 GGAGGAAGGCGAGGATGACG 1197

RESULT 10
AAV66848
ID AAV66848 standard; DNA; 1548 BP.
XX
AC AAV66848;
XX
DT 17-OCT-2003 (revised)
DT 06-JAN-1999 (first entry)
XX
DE Chlamydia 16S ribosome RNA gene #4.
XX
KW Chlamydia genus; microbe; bird-hosted; 16S ribosome RNA; detection; ds.
XX
OS Chlamydophila caviae.
XX
PN JP10262679-A.
XX
PD 06-OCT-1998.
XX
PF 28-MAR-1997; 97JP-00078591.
XX
PR 28-MAR-1997; 97JP-00078591.
XX
PA (ATAT-) A & T KK.
PA (TOKU) TOKUYAMA SODA KK.
XX
DR WPI; 1998-587294/50.
XX
PT Chlamydia species ribosome genes, and primers derived from it - used for
PT the nucleic acid amplification detection of Chlamydia species.
XX
PS Claim 1; Page 14-15; 18pp; Japanese.
XX
CC The present sequence represents a gene coding Chlamydia 16s ribosome RNA
CC from Chlamydia psittaci. Also described in the present invention are: (1)
CC a recombinant vector containing the above gene; and (2) a transformant
CC transformed by the above recombinant vector. The nucleic acid, and
CC primers which can hybridise to it, are used for the specific nucleic acid
CC amplification detection of a Chlamydia genus microbe i.e. detection of
CC PCR products. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 1548 BP; 410 A; 328 C; 452 G; 358 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 1548;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAAGGCGAGGATGACG 20
||||||||||||||||||||
Db 1178 GGAGGAAGGCGAGGATGACG 1197

RESULT 11
AAV66845
ID AAV66845 standard; DNA; 1548 BP.
XX
AC AAV66845;
XX
DT 17-OCT-2003 (revised)
DT 06-JAN-1999 (first entry)
XX
DE Chlamydia 16S ribosome RNA gene #1.
XX
KW Chlamydia genus; microbe; bird-hosted; 16S ribosome RNA; detection; ds.
XX
OS Chlamydophila caviae.
XX
PN JP10262679-A.
XX
PD 06-OCT-1998.
XX
PF 28-MAR-1997; 97JP-00078591.
XX
PR 28-MAR-1997; 97JP-00078591.
XX
PA (ATAT-) A & T KK.
PA (TOKU) TOKUYAMA SODA KK.
XX
DR WPI; 1998-587294/50.
XX
PT Chlamydia species ribosome genes, and primers derived from it - used for
PT the nucleic acid amplification detection of Chlamydia species.
XX
PS Claim 1; Page 13; 18pp; Japanese.
XX
CC The present sequence represents a gene coding Chlamydia 16s ribosome RNA
CC from Chlamydia psittaci. Also described in the present invention are: (1)
CC a recombinant vector containing the above gene; and (2) a transformant
CC transformed by the above recombinant vector. The nucleic acid, and
CC primers which can hybridise to it, are used for the specific nucleic acid
CC amplification detection of a Chlamydia genus microbe i.e. detection of
CC PCR products. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 1548 BP; 413 A; 323 C; 453 G; 359 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 1548;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAGGAAGGCGAGGATGACG 20
              ||||||||||||||||||||
Db       1178 GGAGGAAGGCGAGGATGACG 1197
```

RESULT 12
AAV66850
ID AAV66850 standard; DNA; 1548 BP.
XX
AC AAV66850;
XX
DT 06-JAN-1999 (first entry)
XX
DE Chlamydia 16S ribosome RNA gene #6.
XX
KW Chlamydia genus; microbe; bird-hosted; 16S ribosome RNA; detection; ds.
XX
OS Chlamydia trachomatis.
XX
PN JP10262679-A.
XX
PD 06-OCT-1998.
XX
PF 28-MAR-1997; 97JP-00078591.
XX
PR 28-MAR-1997; 97JP-00078591.
XX
PA (ATAT-) A & T KK.
PA (TOKU) TOKUYAMA SODA KK.
XX
DR WPI; 1998-587294/50.
XX
PT Chlamydia species ribosome genes, and primers derived from it - used for
PT the nucleic acid amplification detection of Chlamydia species.
XX
PS Claim 1; Page 16; 18pp; Japanese.
XX
CC The present sequence represents a gene coding Chlamydia 16s ribosome RNA
CC from Chlamydia trachomatis. Also described in the present invention are:
CC (1) a recombinant vector containing the above gene; and (2) a
CC transformant transformed by the above recombinant vector. The nucleic
CC acid, and primers which can hybridise to it, are used for the specific
CC nucleic acid amplification detection of a Chlamydia genus microbe i.e.
CC detection of PCR products
XX
SQ Sequence 1548 BP; 402 A; 326 C; 470 G; 350 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 1548;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAGGAAGGCGAGGATGACG 20
              ||||||||||||||||||||
Db       1179 GGAGGAAGGCGAGGATGACG 1198
```

RESULT 13
AAV66847
ID AAV66847 standard; DNA; 1548 BP.
XX
AC AAV66847;
XX
DT 17-OCT-2003 (revised)
DT 06-JAN-1999 (first entry)
XX
DE Chlamydia 16S ribosome RNA gene #3.
XX
KW Chlamydia genus; microbe; bird-hosted; 16S ribosome RNA; detection; ds.
XX
OS Chlamydophila caviae.
XX
PN JP10262679-A.
XX
PD 06-OCT-1998.
XX
PF 28-MAR-1997; 97JP-00078591.
XX
PR 28-MAR-1997; 97JP-00078591.
XX
PA (ATAT-) A & T KK.
PA (TOKU) TOKUYAMA SODA KK.
XX
DR WPI; 1998-587294/50.
XX
PT Chlamydia species ribosome genes, and primers derived from it - used for
PT the nucleic acid amplification detection of Chlamydia species.
XX
PS Claim 1; Page 14; 18pp; Japanese.
XX
CC The present sequence represents a gene coding Chlamydia 16s ribosome RNA
CC from Chlamydia psittaci. Also described in the present invention are: (1)
CC a recombinant vector containing the above gene; and (2) a transformant
CC transformed by the above recombinant vector. The nucleic acid, and
CC primers which can hybridise to it, are used for the specific nucleic acid
CC amplification detection of a Chlamydia genus microbe i.e. detection of
CC PCR products. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 1548 BP; 415 A; 328 C; 451 G; 354 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 1548;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAGGAAGGCGAGGATGACG 20
              ||||||||||||||||||||
Db       1178 GGAGGAAGGCGAGGATGACG 1197
```

RESULT 14
AAS11031
ID AAS11031 standard; DNA; 1548 BP.
XX
AC AAS11031;
XX
DT 06-AUG-2003 (revised)
DT 24-OCT-2001 (first entry)
XX
DE Chlamydia trachomytis 16s ribosomal RNA gene.
XX
KW Antisense; bacterial 16s ribosomal RNA; rRNA; bacterial infection; human;
KW food grain supplement; livestock; poultry; therapeutic; ds.
XX
OS Chlamydia trachomatis.
XX
PN WO200142457-A2.
XX
PD 14-JUN-2001.
XX
PF 29-NOV-2000; 2000WO-US042391.
XX
PR 29-NOV-1999; 99US-0168150P.
XX
PA (AVIB-) AVI BIOPHARMA INC.
XX
PI Iversen PL;
XX
DR WPI; 2001-457295/49.
XX
PT Antibacterial compound, useful for treating bacterial infections and as
PT livestock and poultry food supplement, comprises antisense
PT oligonucleotides complementary to bacterial 16S and 23S rRNA.
XX
PS Disclosure; Page; 62pp; English.
XX
CC AAS11021-AAS11034 represent the coding sequences of bacterial 16s
CC ribosomal RNA (rRNA) genes. The sequences were used to design anti-

CC bacterial compounds comprising substantially uncharged antisense
CC oligomers containing 8-40 nucleotide subunits, including a targeting
CC nucleic acid sequence at least 10 nucleotides in length which is
CC complementary to a bacterial 16S or 23S rRNA nucleic acid sequence. The
CC antisense oligomers are used for treating a bacterial infection in a
CC human or a mammalian animal produced by Escherichia coli, Salmonella
CC typhimurium, Pseudomonas aeruginosa, Vibrio cholera, Neisseria
CC gonorrhoea, Helicobacter pylori, Bartonella henselae, Haemophilus
CC influenza, Shigella dysenterae, Staphylococcus aureus, Mycobacterium
CC tuberculosis, Streptococcus pneumoniae, Treponema palladium and Chlamydia
CC trachomatis. The antibacterial compound may be used as a food grain
CC supplement in livestock and poultry food composition. Note: The present
CC sequence is not shown in the specification but has been accessed from
CC GenBank using the appropriate accession number given in the
CC specification. (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ Sequence 1548 BP; 402 A; 327 C; 468 G; 351 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 5; Length 1548;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAAGGCGAGGATGACG 20
||||||||||||||||||||
Db 1179 GGAGGAAGGCGAGGATGACG 1198

RESULT 15
AAV66851
ID AAV66851 standard; DNA; 1549 BP.
XX
AC AAV66851;
XX
DT 06-JAN-1999 (first entry)
XX
DE Chlamydia 16S ribosome RNA gene #7.
XX
KW Chlamydia genus; microbe; bird-hosted; 16S ribosome RNA; detection; ds.
XX
OS Chlamydia trachomatis.
XX
PN JP10262679-A.
XX
PD 06-OCT-1998.
XX
PF 28-MAR-1997; 97JP-00078591.
XX
PR 28-MAR-1997; 97JP-00078591.
XX
PA (ATAT-) A & T KK.
PA (TOKU) TOKUYAMA SODA KK.
XX
DR WPI; 1998-587294/50.
XX
PT Chlamydia species ribosome genes, and primers derived from it - used for
PT the nucleic acid amplification detection of Chlamydia species.
XX
PS Claim 1; Page 16-17; 18pp; Japanese.
XX
CC The present sequence represents a gene coding Chlamydia 16s ribosome RNA
CC from Chlamydia trachomatis. Also described in the present invention are:
CC (1) a recombinant vector containing the above gene; and (2) a
CC transformant transformed by the above recombinant vector. The nucleic
CC acid, and primers which can hybridise to it, are used for the specific
CC nucleic acid amplification detection of a Chlamydia genus microbe i.e.
CC detection of PCR products
XX
SQ Sequence 1549 BP; 402 A; 326 C; 470 G; 351 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 1549;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAAGGCGAGGATGACG 20
||||||||||||||||||||
Db 1179 GGAGGAAGGCGAGGATGACG 1198

Search completed: August 4, 2004, 06:43:35
Job time : 166.337 secs

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 05:41:25 ; Search time 1393.25 Seconds
(without alignments)
428.668 Million cell updates/sec

Title: US-09-940-860-1
Perfect score: 20
Sequence: 1 gcaaacaggattagataccc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	20	100.0	122	9	AI903353	AI903353 RC-BT029-
2	20	100.0	133	10	BE084285	BE084285 PM3-BT065
c 3	20	100.0	168	14	CF199424	CF199424 EST1023 T
4	20	100.0	174	14	CD088408	CD088408 MC1-0050T
c 5	20	100.0	186	10	AW947763	AW947763 RC0-MT000
6	20	100.0	205	14	CD164995	CD164995 ML1-0093T
7	20	100.0	214	14	H74424	H74424 126 Standar
c 8	20	100.0	221	9	AT000468	AT000468 AT000468
9	20	100.0	243	28	BH831104	BH831104 BACPP32-L
10	20	100.0	248	14	CF338988	CF338988 RCL1--03-
11	20	100.0	275	13	BX000722	BX000722 BX000722
c 12	20	100.0	297	12	BG874702	BG874702 CM0-BN007
c 13	20	100.0	301	12	BG874706	BG874706 CM3-BN007
c 14	20	100.0	312	9	AI903266	AI903266 RC-BT029-
c 15	20	100.0	312	9	AI903386	AI903386 RC-BT029-
c 16	20	100.0	312	9	AI903431	AI903431 RC-BT029-
c 17	20	100.0	312	9	AI903433	AI903433 RC-BT029-
18	20	100.0	332	12	BI742715	BI742715 kx34d02.y
19	20	100.0	335	9	AI903432	AI903432 RC-BT029-
c 20	20	100.0	335	10	BF810332	BF810332 RC6-CI000
21	20	100.0	338	9	AI903307	AI903307 RC-BT029-
c 22	20	100.0	343	12	BG875496	BG875496 PM3-BT065
c 23	20	100.0	350	10	BF810203	BF810203 RC6-CI000
24	20	100.0	366	12	BG987045	BG987045 PM0-HT116
25	20	100.0	368	9	AI903306	AI903306 RC-BT029-
26	20	100.0	373	12	BG988274	BG988274 PM0-HT116
27	20	100.0	375	14	CD097562	CD097562 ME1-0016T
c 28	20	100.0	382	10	BF810198	BF810198 RC6-CI000
29	20	100.0	382	14	CD164371	CD164371 ML1-0087T
30	20	100.0	391	10	BE427958	BE427958 MTD001-1.
31	20	100.0	394	28	BH819649	BH819649 BACPP13-M
c 32	20	100.0	399	10	BF910944	BF910944 CM1-UT003
c 33	20	100.0	407	13	BQ352721	BQ352721 MR1-HT085
c 34	20	100.0	409	10	AW804622	AW804622 QV0-UM009
c 35	20	100.0	425	12	BG874668	BG874668 PM3-BN006
36	20	100.0	437	28	BH835798	BH835798 BACPP9-A0
37	20	100.0	440	9	AU284247	AU284247 AU284247
38	20	100.0	447	12	BM130023	BM130023 pb25c10.y
39	20	100.0	447	12	BM130070	BM130070 pb26b03.y
c 40	20	100.0	454	14	CD091084	CD091084 MC1-0084U
41	20	100.0	464	14	CD032934	CD032934 mgmt011xB
42	20	100.0	465	12	BG357866	BG357866 OV2_31_C0
43	20	100.0	470	12	BI744229	BI744229 pb06b08.y
44	20	100.0	473	28	BH831257	BH831257 BACPP33-C
c 45	20	100.0	476	9	AU165135	AU165135 AU165135

ALIGNMENTS

RESULT 1
AI903353/c
LOCUS AI903353 122 bp mRNA linear EST 30-MAR-2000
DEFINITION RC-BT029-100199-113_1 BT029 Homo sapiens cDNA, mRNA sequence.
ACCESSION AI903353
VERSION AI903353.1 GI:6493740
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 122)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

```
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/seq/gethtml.pl?t1=RC&t2=RC-BT029-113_1.ht
            ml&t3=100199&t4=1)
            Seq primer: puc 18 forward.
FEATURES              Location/Qualifiers
     source           1. .122
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /sex="female"
                      /dev_stage="Adult"
                      /clone_lib="BT029"
                      /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
                      SmaI; A mini-library was made by cloning products derived
                      from  ORESTES PCR (U.S. Letters Patent application No.
                      196,716 -  Ludwig Institute for Cancer Research) profiles
                      into  the pUC 18 vector. Reverse transcription of tissue
                      mRNA and cDNA amplification were performed under low
                      stringency conditions."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 9;  Length 122;
  Best Local Similarity   100.0%;  Pred. No. 0.078;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db        100 GCAAACAGGATTAGATACCC 81


RESULT 2
BE084285
LOCUS       BE084285                133 bp    mRNA    linear   EST 12-JUN-2000
DEFINITION  PM3-BT0654-030300-002-d12 BT0654 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE084285
VERSION     BE084285.1  GI:8474639
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 133)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=PM3-BT0654-030
            300-002-d12&t3=2000-03-03&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 17
            High quality sequence stop: 133.
FEATURES              Location/Qualifiers
     source           1. .133
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /dev_stage="Adult"
                      /clone_lib="BT0654"
                      /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
                      SmaI; A mini-library was made by cloning products derived
                      from  ORESTES PCR (U.S. Letters Patent application No.
                      196,716 -  Ludwig Institute for Cancer Research) profiles
                      into  the pUC 18 vector. Reverse transcription of tissue
                      mRNA and cDNA amplification were performed under low
                      stringency conditions."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 10;  Length 133;
  Best Local Similarity   100.0%;  Pred. No. 0.079;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         21 GCAAACAGGATTAGATACCC 40


RESULT 3
CF199424/c
LOCUS       CF199424                168 bp    mRNA    linear   EST 01-AUG-2003
DEFINITION  EST1023 Tamarix androssowii leaf Tamarix androssowii cDNA, mRNA
            sequence.
ACCESSION   CF199424
VERSION     CF199424.1  GI:33393797
KEYWORDS    EST.
SOURCE      Tamarix androssowii
  ORGANISM  Tamarix androssowii
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Tamaricaceae; Tamarix.
REFERENCE   1  (bases 1 to 168)
  AUTHORS   Wang,Y., Yang,C., Jiang,J., Liu,G., Wu,J. and Liu,Z.
  TITLE     EST aquired from cDNA library of Tamarix androssowii treated with
            NaHCO3
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Yucheng Wang
            Forestry Source and Environment College
            Northeast Forestry University
            Hexing 26, Harbin, Heilongjiang, 150040, P.R. China
            Tel: 086-451-2190607
            Email: WANGYUCHENG1029@YAHOO.COM.CN.
FEATURES              Location/Qualifiers
     source           1. .168
                      /organism="Tamarix androssowii"
                      /mol_type="mRNA"
                      /db_xref="taxon:189785"
                      /tissue_type="leaf"
                      /clone_lib="Tamarix androssowii leaf"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 14;  Length 168;
  Best Local Similarity   100.0%;  Pred. No. 0.081;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db        108 GCAAACAGGATTAGATACCC 89


RESULT 4
CD088408
LOCUS       CD088408                174 bp    mRNA    linear   EST 14-SEP-2003
DEFINITION  MC1-0050T-R112-C03-U.G MC1-0050 Schistosoma mansoni cDNA clone
            MC1-0050T-R112-C03.G, mRNA sequence.
ACCESSION   CD088408
```

VERSION CD088408.1 GI:34639304
KEYWORDS EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE 1 (bases 1 to 174)
AUTHORS Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M., Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr., Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F., Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L., Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A., Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A., Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T., Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M., Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
TITLE Transcriptome analysis of the acoelomate human parasite Schistosoma mansoni
JOURNAL Nat. Genet. 35 (2), 148-157 (2003)
MEDLINE 22879926
COMMENT Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquimica
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP, Brasil
Tel: +55-11-3091-2173
Fax: +55-11-3091-2186
Email: verjo@iq.usp.br
This sequence was derived from the FAPESP Schistosoma mansoni EST Genome Project. All sequences in the project were assembled and annotated. This entry and all the assembled sequences can be seen in the following URL http://bioinfo.iq.usp.br/schisto/
Plate: MC1-0050T-R112 row: 3 column: C.
FEATURES Location/Qualifiers
source 1. .174
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="MC1-0050T-R112-C03.G"
/sex="mixed pool"
/dev_stage="cercaria"
/lab_host="Biomphalaria glabrata"
/clone_lib="MC1-0050"
/note="Vector: pGEM T-easy"
ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         74 GCAAACAGGATTAGATACCC 93
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RESULT 5
AW947763/c
LOCUS AW947763 186 bp mRNA linear EST 31-MAY-2000
DEFINITION RC0-MT0006-110300-021-d10 MT0006 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW947763
VERSION AW947763.1 GI:8125537
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 186)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=RC0-MT0006-110300-021-d10&t3=2000-03-11&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 20
High quality sequence stop: 186.
FEATURES Location/Qualifiers
source 1. .186
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="MT0006"
/note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 186;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db        101 GCAAACAGGATTAGATACCC 82
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RESULT 6
CD164995
LOCUS CD164995 205 bp mRNA linear EST 14-SEP-2003
DEFINITION ML1-0093T-D139-B11-U.G ML1-0093 Schistosoma mansoni cDNA clone ML1-0093T-D139-B11.G, mRNA sequence.
ACCESSION CD164995
VERSION CD164995.1 GI:34701658
KEYWORDS EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE 1 (bases 1 to 205)
AUTHORS Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M., Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr., Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F., Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L., Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A., Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A., Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T., Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M., Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
TITLE Transcriptome analysis of the acoelomate human parasite Schistosoma mansoni
JOURNAL Nat. Genet. 35 (2), 148-157 (2003)
MEDLINE 22879926
COMMENT Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquimica

Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP, Brasil
Tel: +55-11-3091-2173
Fax: +55-11-3091-2186
Email: verjo@iq.usp.br
This sequence was derived from the FAPESP Schistosoma mansoni EST Genome Project. All sequences in the project were assembled and annotated. This entry and all the assembled sequences can be seen in the following URL http://bioinfo.iq.usp.br/schisto/
Plate: ML1-0093T-D139 row: 11 column: B.

FEATURES Location/Qualifiers
source 1. .205
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="ML1-0093T-D139-B11.G"
/sex="mixed pool"
/dev_stage="miracidium"
/clone_lib="ML1-0093"
/note="Vector: pGEM T-easy"

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 205;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 57 GCAAACAGGATTAGATACCC 76

RESULT 7
H74424
LOCUS H74424 214 bp mRNA linear EST 31-OCT-1995
DEFINITION 126 Standard Brassica napus cDNA clone R185F, mRNA sequence.
ACCESSION H74424
VERSION H74424.1 GI:1048331
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 214)
AUTHORS Park,Y.S., Kwak,J.M., Kwon,O.Y., Kim,Y.S., Lee,D.S., Cho,M.J., Lee,H.H. and Nam,H.G.
TITLE Generation of expressed sequence tags of random root cDNA clones of Brassica napus by single-run partial sequencing
JOURNAL Plant Physiol. 103, 359-370 (1993)
MEDLINE 94302145
PUBMED 8029332
COMMENT Contact: Nam, HG
Plant Molecular Genetics Laboratory
Pohang University of Science and Technology
Dept. of Life Science, San31 Hyojadong, Pohang Kyungbuk 790-784, Korea
Tel: 825622792111
Fax: 825622792199
Email: nam@vision.postech.ac.kr
Seq primer: M13 forward.

FEATURES Location/Qualifiers
source 1. .214
/organism="Brassica napus"
/mol_type="mRNA"
/strain="L. cv Naehan"
/db_xref="taxon:3708"
/clone="R185F"
/lab_host="E. coli DH5a"
/clone_lib="Standard"
/note="Vector: pUC19; Site_1: EcoRI; Site_2: EcoRI; ESTs were generated from the root cDNA library of Brassica napus. The cDNA was synthesized from root poly(A) RNA with Pharmacia's cDNA synthesis kit using oligo(dT) as a primer. The Eco RI/Not I adaptor was ligated to the dsDNA. The cDNAs inserts were cloned into the pUC19 vector digested with EcoRI."

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 124 GCAAACAGGATTAGATACCC 143

RESULT 8
AT000468/c
LOCUS AT000468 221 bp mRNA linear EST 13-AUG-1998
DEFINITION AT000468 Brassica rapa guard cell Brassica rapa subsp. pekinensis cDNA clone DGT85, mRNA sequence.
ACCESSION AT000468
VERSION AT000468.1 GI:3414002
KEYWORDS EST.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 221)
AUTHORS Kwak,J.M., Kim,S.A., Hong,S.W. and Nam,H.G.
TITLE Evaluation of 515 expressed sequence tags obtained from guard cells of Brassica campestris
JOURNAL Planta 202 (1), 9-17 (1997)
MEDLINE 97320163
PUBMED 9177047
COMMENT Contact: Hong-Gil Nam
Department of Life Science, Plant Molecular Genetics Laboratory
Pohang University of Science and Technology
San 31 Hyojadong, Pohang Kyungbuk 790-784, Korea
Email: hgn@bric.postech.ac.kr
Submitted through BRIC(Biological Research Information Center) of Korea URL: http://bric.postech.ac.kr/.

FEATURES Location/Qualifiers
source 1. .221
/organism="Brassica rapa subsp. pekinensis"
/mol_type="mRNA"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="DGT85"
/cell_type="guard cell protoplast"
/clone_lib="Brassica rapa guard cell"

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 221;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 119 GCAAACAGGATTAGATACCC 100

RESULT 9
BH831104
LOCUS BH831104 243 bp DNA linear GSS 20-MAY-2002
DEFINITION BACPP32-L04.z Pristionchus pacificus BAC ends Pristionchus pacificus genomic, genomic survey sequence.
ACCESSION BH831104
VERSION BH831104.1 GI:21028448
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

```
            Neodiplogasteridae; Pristionchus.
REFERENCE   1  (bases 1 to 243)
  AUTHORS   Srinivasan,J., Sinz,W., Lanz,C., Brand,A., Nandakumar,R.,
            Raddatz,G., Witte,H., Keller,H., Kipping,I., Pires da Silva,A.,
            Jesse,T., Millare,J., de Both,M., Schuster,S.C. and Sommer,R.J.
  TITLE     A BAC-based genetic linkage map of the nematode Pristionchus
            pacificus
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .243
                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="var. California"
                     /db_xref="taxon:54126"
                     /clone_lib="Pristionchus pacificus BAC ends"
ORIGIN

  Query Match           100.0%;  Score 20;  DB 28;  Length 243;
  Best Local Similarity  100.0%;  Pred. No. 0.084;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db        121 GCAAACAGGATTAGATACCC 140


RESULT 10
CF338988
LOCUS       CF338988                248 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  RCL1--03-G23.g1 Regenerated callus lambda phage cDNA library (RCL1)
            Oryza sativa cDNA clone RCL1--03-G23, mRNA sequence.
ACCESSION   CF338988
VERSION     CF338988.1  GI:33826360
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 248)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .248
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="RCL1--03-G23"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli SOLR"
                     /clone_lib="Regenerated callus lambda phage cDNA library
                     (RCL1)"
                     /note="Vector: pBluescript SK(+); Site_1: SstI; Site_2:
                     XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
                     end with SstI and 3' end with XhoI site. Callus was
                     induced on 2N6 media for 30 days and cultured for 36hrs on
                     regenerated media"
ORIGIN

  Query Match           100.0%;  Score 20;  DB 14;  Length 248;
  Best Local Similarity  100.0%;  Pred. No. 0.084;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db        159 GCAAACAGGATTAGATACCC 178


RESULT 11
BX000722
LOCUS       BX000722                275 bp    mRNA    linear   EST 03-DEC-2002
DEFINITION  BX000722 Pinus pinaster xylem Pinus pinaster cDNA clone PPEM56,
            mRNA sequence.
ACCESSION   BX000722
VERSION     BX000722.1  GI:26020290
KEYWORDS    EST.
SOURCE      Pinus pinaster
  ORGANISM  Pinus pinaster
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE   1  (bases 1 to 275)
  AUTHORS   Le Provost,G., Paiva,J., Pot,D., Brach,J. and Plomion,P.
  TITLE     Seasonal variation in transcript accumulation in wood forming
            tissue of maritime pine (Pinus pinaster Ait.) with emphasis on a
            cell wall Glycine Rich Protein
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Frigerio JM
            Genetique et Amelioration 69
            INRA
            route d'Arcachon 33612 Cestas CEDEX France
            Email: Frigerio@pierroton.inra.fr.
FEATURES             Location/Qualifiers
     source          1. .275
                     /organism="Pinus pinaster"
                     /mol_type="mRNA"
                     /db_xref="taxon:71647"
                     /clone="PPEM56"
                     /tissue_type="xylem"
                     /clone_lib="Pinus pinaster xylem"
                     /note="Compression wood was induced in four 14-year old
                     maritime pine clones by artifitial bending. Control clone
                     (no bending) were sampled for xylem associated with early
                     wood and late wood at the beginning (April) and at the end
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                     corresponding to Early wood, late wood, compression wood
                     and opposite wood were used for mRNA fingerprinting using
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ORIGIN

  Query Match           100.0%;  Score 20;  DB 13;  Length 275;
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RESULT 12
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LOCUS       BG874702                297 bp    mRNA    linear   EST 30-MAY-2001
DEFINITION  CM0-BN0075-220200-237-h05 BN0075 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG874702
VERSION     BG874702.1  GI:14251633
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 297)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=CM0-BN0075-220
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            Seq primer: puc 18 forward
            High quality sequence start: 17
            High quality sequence stop: 297.
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                     /clone_lib="BN0075"
                     /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

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RESULT 13
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LOCUS       BG874706                301 bp    mRNA    linear   EST 30-MAY-2001
DEFINITION  CM3-BN0075-240200-101-h05 BN0075 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG874706
VERSION     BG874706.1  GI:14251637
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=CM3-BN0075-240
            200-101-h05&t3=2000-02-24&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 19
            High quality sequence stop: 301.
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                     /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

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RESULT 14
AI903266/c
LOCUS       AI903266                312 bp    mRNA    linear   EST 30-MAR-2000
DEFINITION  RC-BT029-070199-018 BT029 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AI903266
VERSION     AI903266.1  GI:6493653
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 312)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
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            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
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            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/seq/gethtml.pl?t1=RC&t2=RC-BT029-018.html
            &t3=070199&t4=1)
            Seq primer: puc 18 forward.
FEATURES              Location/Qualifiers
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                      /sex="female"
                      /dev_stage="Adult"
                      /clone_lib="BT029"
                      /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
                      SmaI; A mini-library was made by cloning products derived
                      from  ORESTES PCR (U.S. Letters Patent application No.
                      196,716 -  Ludwig Institute for Cancer Research) profiles
                      into  the pUC 18 vector. Reverse transcription of tissue
                      mRNA and cDNA amplification were performed under low
                      stringency conditions."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 9;  Length 312;
  Best Local Similarity   100.0%;  Pred. No. 0.086;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        100 GCAAACAGGATTAGATACCC 81


RESULT 15
AI903386/c
LOCUS       AI903386                312 bp    mRNA    linear   EST 30-MAR-2000
DEFINITION  RC-BT029-110199-165 BT029 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AI903386
VERSION     AI903386.1  GI:6493773
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 312)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/seq/gethtml.pl?t1=RC&t2=RC-BT029-165.html
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            Seq primer: puc 18 forward.
FEATURES              Location/Qualifiers
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                      /clone_lib="BT029"
                      /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
                      SmaI; A mini-library was made by cloning products derived
                      from  ORESTES PCR (U.S. Letters Patent application No.
                      196,716 -  Ludwig Institute for Cancer Research) profiles
                      into  the pUC 18 vector. Reverse transcription of tissue
                      mRNA and cDNA amplification were performed under low
                      stringency conditions."
ORIGIN

  Query Match             100.0%;  Score 20;  DB 9;  Length 312;
  Best Local Similarity   100.0%;  Pred. No. 0.086;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
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Db        100 GCAAACAGGATTAGATACCC 81


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GenCore version 5.1.6

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	20	100.0	25	17	US-09-283-655-1	Sequence 1, Appli
3	20	100.0	25	26	US-09-620-375-1	Sequence 1, Appli
4	20	100.0	25	54	US-10-715-220-1	Sequence 1, Appli
5	20	100.0	30	39	US-09-940-860-6	Sequence 6, Appli
c 6	20	100.0	47	6	US-08-246-935-2	Sequence 2, Appli
7	20	100.0	50	49	US-10-343-319-76	Sequence 76, Appl
8	20	100.0	50	49	US-10-343-319-77	Sequence 77, Appl
9	20	100.0	50	49	US-10-343-319-79	Sequence 79, Appl
10	20	100.0	50	49	US-10-343-319-80	Sequence 80, Appl
11	20	100.0	50	49	US-10-343-319-81	Sequence 81, Appl
12	20	100.0	50	49	US-10-343-319-82	Sequence 82, Appl
13	20	100.0	50	49	US-10-343-319-83	Sequence 83, Appl
14	20	100.0	50	49	US-10-343-319-84	Sequence 84, Appl
15	20	100.0	50	49	US-10-343-319-85	Sequence 85, Appl
16	20	100.0	50	49	US-10-343-319-87	Sequence 87, Appl
17	20	100.0	50	49	US-10-343-319-88	Sequence 88, Appl
18	20	100.0	50	49	US-10-343-319-89	Sequence 89, Appl
19	20	100.0	50	49	US-10-343-319-90	Sequence 90, Appl
20	20	100.0	50	49	US-10-343-319-91	Sequence 91, Appl
21	20	100.0	50	49	US-10-343-319-98	Sequence 98, Appl
22	20	100.0	50	49	US-10-343-319-99	Sequence 99, Appl
23	20	100.0	50	49	US-10-343-319-102	Sequence 102, App
24	20	100.0	50	49	US-10-343-319-104	Sequence 104, App
25	20	100.0	50	49	US-10-343-319-105	Sequence 105, App
26	20	100.0	105	51	US-10-415-182A-337	Sequence 337, App
27	20	100.0	237	11	US-08-731-034-686	Sequence 686, App
28	20	100.0	237	56	US-60-004-674-686	Sequence 686, App
29	20	100.0	248	11	US-08-731-034-37	Sequence 37, Appl
30	20	100.0	248	56	US-60-004-674-37	Sequence 37, Appl
c 31	20	100.0	279	51	US-10-417-884-3170	Sequence 3170, Ap
c 32	20	100.0	279	51	US-10-417-884-3171	Sequence 3171, Ap
33	20	100.0	293	51	US-10-410-040A-19	Sequence 19, Appl
34	20	100.0	294	51	US-10-410-040A-15	Sequence 15, Appl
35	20	100.0	294	51	US-10-410-040A-16	Sequence 16, Appl
36	20	100.0	294	51	US-10-410-040A-17	Sequence 17, Appl
37	20	100.0	294	51	US-10-410-040A-18	Sequence 18, Appl
38	20	100.0	294	51	US-10-410-040A-20	Sequence 20, Appl
39	20	100.0	294	51	US-10-410-040A-21	Sequence 21, Appl
40	20	100.0	294	51	US-10-410-040A-23	Sequence 23, Appl
c 41	20	100.0	306	15	US-09-107-433-2236	Sequence 2236, Ap
c 42	20	100.0	306	53	US-10-617-320-2236	Sequence 2236, Ap
43	20	100.0	352	58	US-60-029-960-1510	Sequence 1510, Ap
44	20	100.0	375	27	US-09-652-913-6226	Sequence 6226, Ap
45	20	100.0	413	20	US-09-465-877-1662	Sequence 1662, Ap

ALIGNMENTS

```
RESULT 1
US-09-940-860-1
; Sequence 1, Application US/09940860
; GENERAL INFORMATION:
;  APPLICANT: Rothman, Richard
;  APPLICANT:  Majmudar, Maulik
;  TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
;  FILE REFERENCE: 01107.00185
;  CURRENT APPLICATION NUMBER: US/09/940,860
;  CURRENT FILING DATE:  2001-08-29
;  PRIOR APPLICATION NUMBER: 60/229,376
;  PRIOR FILING DATE: 2000-08-31
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic amplification primer
US-09-940-860-1

  Query Match           100.0%;  Score 20;  DB 39;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db          1 GCAAACAGGATTAGATACCC 20


RESULT 2
US-09-283-655-1
; Sequence 1, Application US/09283655
; GENERAL INFORMATION:
;  APPLICANT: Vojdani, A.
;  TITLE OF INVENTION: DETECTION OF MYCOPLASMA IN PATIENTS WITH
;  TITLE OF INVENTION: CHRONIC FATIGUE SYNDROME AND RELATED DISORDERS
;  FILE REFERENCE: IMSCI.009A
;  CURRENT APPLICATION NUMBER: US/09/283,655
;  CURRENT FILING DATE: 1999-04-01
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide primer
US-09-283-655-1

  Query Match           100.0%;  Score 20;  DB 17;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db          5 GCAAACAGGATTAGATACCC 24


RESULT 3
US-09-620-375-1
; Sequence 1, Application US/09620375
; GENERAL INFORMATION:
;  APPLICANT: Vojdani, A.
;  TITLE OF INVENTION: DETECTION OF MYCOPLASMA IN PATIENTS WITH
;  TITLE OF INVENTION:  CHRONIC FATIGUE SYNDROME AND RELATED DISORDERS
;  FILE REFERENCE: IMSCI.009A
;  CURRENT APPLICATION NUMBER: US/09/620,375
;  CURRENT FILING DATE:  2000-07-20
;  PRIOR APPLICATION NUMBER: 09/283,655
;  PRIOR FILING DATE: 1999-04-02
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide primer
US-09-620-375-1

  Query Match           100.0%;  Score 20;  DB 26;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db          5 GCAAACAGGATTAGATACCC 24


RESULT 4
```

```
US-10-715-220-1
; Sequence 1, Application US/10715220
; GENERAL INFORMATION:
;  APPLICANT: Vojdani, A.
;  TITLE OF INVENTION: DETECTION OF MYCOPLASMA IN PATIENTS WITH
;  TITLE OF INVENTION:  CHRONIC FATIGUE SYNDROME AND RELATED DISORDERS
;  FILE REFERENCE: IMSCI.009A
;  CURRENT APPLICATION NUMBER: US/10/715,220
;  CURRENT FILING DATE:  2003-11-17
;  PRIOR APPLICATION NUMBER: US/09/283,655
;  PRIOR FILING DATE: 1999-04-01
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide primer
US-10-715-220-1

  Query Match             100.0%;  Score 20;  DB 54;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db          5 GCAAACAGGATTAGATACCC 24


RESULT 5
US-09-940-860-6
; Sequence 6, Application US/09940860
; GENERAL INFORMATION:
;  APPLICANT: Rothman, Richard
;  APPLICANT:  Majmudar, Maulik
;  TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
;  FILE REFERENCE: 01107.00185
;  CURRENT APPLICATION NUMBER: US/09/940,860
;  CURRENT FILING DATE:  2001-08-29
;  PRIOR APPLICATION NUMBER: 60/229,376
;  PRIOR FILING DATE: 2000-08-31
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic amplification primer
US-09-940-860-6

  Query Match             100.0%;  Score 20;  DB 39;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db          2 GCAAACAGGATTAGATACCC 21


RESULT 6
US-08-246-935-2/c
; Sequence 2, Application US/08246935
;  GENERAL INFORMATION:
;     APPLICANT:  Weisburg, William G.
;     APPLICANT:  Lane, David J.
;     TITLE OF INVENTION:  A METHOD FOR DETECTING AND IDENTIFYING
;     TITLE OF INVENTION:  PATHOGENIC ORGANISMS USING TARGET SEQUENCES AS DETECTORS
;     NUMBER OF SEQUENCES:  3
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;       STREET:  Two Militia Drive
;       CITY:  Lexington
;       STATE:  Massachusetts
;       COUNTRY:  USA
;       ZIP:  02173
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/246,935
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/707,646
;       FILING DATE:  30-MAY-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Granahan, Patricia
;       REGISTRATION NUMBER:  32,227
;       REFERENCE/DOCKET NUMBER:  GTR90-02
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617)861-6240
;       TELEFAX:  (617)861-9540
;  INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  47 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA probe
;     FEATURE:
;       NAME/KEY:  GTS OLIGO NUMBER 1739
US-08-246-935-2

  Query Match             100.0%;  Score 20;  DB 6;  Length 47;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         33 GCAAACAGGATTAGATACCC 14


RESULT 7
US-10-343-319-76
; Sequence 76, Application US/10343319
; GENERAL INFORMATION:
;  APPLICANT: Hunter, Neil
;  APPLICANT:  Jacques, Nicholas A.
;  APPLICANT:  Martin, Fjelda E.
;  APPLICANT:  Nardkani, Mangala A.
;  TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
;  FILE REFERENCE: DAVI139.002APC
;  CURRENT APPLICATION NUMBER: US/10/343,319
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: PCT/AU01/00933
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: AU PQ9090/2000
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Campylobacter jejuni
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Helicobacter pylori also.
US-10-343-319-76

  Query Match             100.0%;  Score 20;  DB 49;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
```

```
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         16 GCAAACAGGATTAGATACCC 35


RESULT 8
US-10-343-319-77
; Sequence 77, Application US/10343319
; GENERAL INFORMATION:
;  APPLICANT: Hunter, Neil
;  APPLICANT:  Jacques, Nicholas A.
;  APPLICANT:  Martin, Fjelda E.
;  APPLICANT:  Nardkani, Mangala A.
;  TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
;  FILE REFERENCE: DAVI139.002APC
;  CURRENT APPLICATION NUMBER: US/10/343,319
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: PCT/AU01/00933
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: AU PQ9090/2000
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 77
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Treponema denticola
US-10-343-319-77

  Query Match           100.0%;  Score 20;  DB 49;  Length 50;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         16 GCAAACAGGATTAGATACCC 35


RESULT 9
US-10-343-319-79
; Sequence 79, Application US/10343319
; GENERAL INFORMATION:
;  APPLICANT: Hunter, Neil
;  APPLICANT:  Jacques, Nicholas A.
;  APPLICANT:  Martin, Fjelda E.
;  APPLICANT:  Nardkani, Mangala A.
;  TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
;  FILE REFERENCE: DAVI139.002APC
;  CURRENT APPLICATION NUMBER: US/10/343,319
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: PCT/AU01/00933
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: AU PQ9090/2000
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 79
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Leptothrix mobilis
US-10-343-319-79

  Query Match           100.0%;  Score 20;  DB 49;  Length 50;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         16 GCAAACAGGATTAGATACCC 35


RESULT 10
US-10-343-319-80
; Sequence 80, Application US/10343319
; GENERAL INFORMATION:
;  APPLICANT: Hunter, Neil
;  APPLICANT:  Jacques, Nicholas A.
;  APPLICANT:  Martin, Fjelda E.
;  APPLICANT:  Nardkani, Mangala A.
;  TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
;  FILE REFERENCE: DAVI139.002APC
;  CURRENT APPLICATION NUMBER: US/10/343,319
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: PCT/AU01/00933
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: AU PQ9090/2000
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 80
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Thiomicrospira denitrificans
US-10-343-319-80

  Query Match           100.0%;  Score 20;  DB 49;  Length 50;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         16 GCAAACAGGATTAGATACCC 35


RESULT 11
US-10-343-319-81
; Sequence 81, Application US/10343319
; GENERAL INFORMATION:
;  APPLICANT: Hunter, Neil
;  APPLICANT:  Jacques, Nicholas A.
;  APPLICANT:  Martin, Fjelda E.
;  APPLICANT:  Nardkani, Mangala A.
;  TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
;  FILE REFERENCE: DAVI139.002APC
;  CURRENT APPLICATION NUMBER: US/10/343,319
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: PCT/AU01/00933
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: AU PQ9090/2000
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 81
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Neisseria meningitidis
US-10-343-319-81

  Query Match           100.0%;  Score 20;  DB 49;  Length 50;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         16 GCAAACAGGATTAGATACCC 35


RESULT 12
US-10-343-319-82
; Sequence 82, Application US/10343319
; GENERAL INFORMATION:
;  APPLICANT: Hunter, Neil
;  APPLICANT:  Jacques, Nicholas A.
;  APPLICANT:  Martin, Fjelda E.
```

```
;  APPLICANT:  Nardkani, Mangala A.
;  TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
;  FILE REFERENCE: DAVI139.002APC
;  CURRENT APPLICATION NUMBER: US/10/343,319
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: PCT/AU01/00933
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: AU PQ9090/2000
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 82
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Actinobacillus actinomycetemcomitans
US-10-343-319-82

  Query Match           100.0%;  Score 20;  DB 49;  Length 50;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         16 GCAAACAGGATTAGATACCC 35


RESULT 13
US-10-343-319-83
; Sequence 83, Application US/10343319
; GENERAL INFORMATION:
;  APPLICANT: Hunter, Neil
;  APPLICANT:  Jacques, Nicholas A.
;  APPLICANT:  Martin, Fjelda E.
;  APPLICANT:  Nardkani, Mangala A.
;  TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
;  FILE REFERENCE: DAVI139.002APC
;  CURRENT APPLICATION NUMBER: US/10/343,319
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: PCT/AU01/00933
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: AU PQ9090/2000
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 83
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Haemophilus influenzae
US-10-343-319-83

  Query Match           100.0%;  Score 20;  DB 49;  Length 50;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         16 GCAAACAGGATTAGATACCC 35


RESULT 14
US-10-343-319-84
; Sequence 84, Application US/10343319
; GENERAL INFORMATION:
;  APPLICANT: Hunter, Neil
;  APPLICANT:  Jacques, Nicholas A.
;  APPLICANT:  Martin, Fjelda E.
;  APPLICANT:  Nardkani, Mangala A.
;  TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
;  FILE REFERENCE: DAVI139.002APC
;  CURRENT APPLICATION NUMBER: US/10/343,319
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: PCT/AU01/00933
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: AU PQ9090/2000
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Escherichia coli
US-10-343-319-84

  Query Match           100.0%;  Score 20;  DB 49;  Length 50;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         16 GCAAACAGGATTAGATACCC 35


RESULT 15
US-10-343-319-85
; Sequence 85, Application US/10343319
; GENERAL INFORMATION:
;  APPLICANT: Hunter, Neil
;  APPLICANT:  Jacques, Nicholas A.
;  APPLICANT:  Martin, Fjelda E.
;  APPLICANT:  Nardkani, Mangala A.
;  TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
;  FILE REFERENCE: DAVI139.002APC
;  CURRENT APPLICATION NUMBER: US/10/343,319
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: PCT/AU01/00933
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: AU PQ9090/2000
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 85
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Salmonella typhi
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Also Vibrio cholerae, Pseudomonas aeruginosa, and
;   OTHER INFORMATION: Rhodospirillum rubrum.
US-10-343-319-85

  Query Match           100.0%;  Score 20;  DB 49;  Length 50;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         16 GCAAACAGGATTAGATACCC 35


Search completed: August  4, 2004, 11:29:48
Job time : 1826.78 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 05:41:25 ; Search time 1393.25 Seconds
(without alignments)
428.668 Million cell updates/sec

Title: US-09-940-860-2
Perfect score: 20
Sequence: 1 ggaggaaggcgaggatgacg 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		18	90.0	304	9	AV295422	AV295422 AV295422
c 2		18	90.0	410	12	BG102240	BG102240 RHIZ2_23_
c 3		18	90.0	508	12	BG380134	BG380134 UI-R-CS0-
4		18	90.0	530	29	CG093861	CG093861 PUFSX26TB
c 5		18	90.0	567	29	CG093863	CG093863 PUFSX26TD
c 6		18	90.0	573	14	CA199884	CA199884 SCRLFL101
c 7		18	90.0	617	14	CA236557	CA236557 SCSBFL501
c 8		18	90.0	784	29	CC657309	CC657309 OGJAO16TV
c 9		18	90.0	784	29	CG734728	CG734728 ZMMBBb029
10		18	90.0	826	10	BE743778	BE743778 601577886
11		18	90.0	867	29	CG458612	CG458612 PUIKZ64TD
c 12		18	90.0	890	28	BZ803618	BZ803618 PUFDX67TD
c 13		18	90.0	951	29	CG038934	CG038934 PUFLB28TD
14		18	90.0	972	29	CG038933	CG038933 PUFLB28TB
15		18	90.0	992	28	BZ803611	BZ803611 PUFDX67TB
16		18	90.0	1013	28	BZ806256	BZ806256 PUGBF03TD
17		17	85.0	242	9	AV319131	AV319131 AV319131
18		17	85.0	245	14	CF771463	CF771463 DSBF1_19_
19		17	85.0	255	9	AV324545	AV324545 AV324545
20		17	85.0	259	14	CA484206	CA484206 WHE4303_E
21		17	85.0	261	14	CA486269	CA486269 WHE4329_D
c 22		17	85.0	268	9	AI438796	AI438796 486013B02
23		17	85.0	273	14	CF760514	CF760514 DSAF1_62_
24		17	85.0	294	10	BB021190	BB021190 BB021190
c 25		17	85.0	303	10	AW202526	AW202526 687038F07
26		17	85.0	314	14	CD226821	CD226821 CCC1_48_H
c 27		17	85.0	317	9	AW066567	AW066567 683002G06
c 28		17	85.0	318	28	BH627207	BH627207 1007069C1
29		17	85.0	322	10	BB040793	BB040793 BB040793
30		17	85.0	330	14	CA485170	CA485170 WHE4315_D
c 31		17	85.0	332	28	BH229295	BH229295 1006151D0
32		17	85.0	337	10	BB131766	BB131766 BB131766
33		17	85.0	338	10	BB161598	BB161598 BB161598
34		17	85.0	338	14	CF758969	CF758969 DSAF1_38_
35		17	85.0	339	14	CF758236	CF758236 DSAF1_29_
36		17	85.0	358	13	BQ282009	BQ282009 WHE3027_H
c 37		17	85.0	360	14	CB603914	CB603914 3529_1_64
38		17	85.0	361	14	CD670294	CD670294 3529_1_13
c 39		17	85.0	374	10	BF457064	BF457064 UI-M-BZ1-
c 40		17	85.0	389	14	CF487372	CF487372 POL1_43_A
41		17	85.0	406	10	AW286184	AW286184 LG1_328_E
c 42		17	85.0	409	12	BM266611	BM266611 MEST383-E
c 43		17	85.0	424	9	AI593552	AI593552 vu55g11.x
c 44		17	85.0	426	9	AI941805	AI941805 618035E02
45		17	85.0	427	10	BF723566	BF723566 mab33f02.

ALIGNMENTS

RESULT 1
AV295422
LOCUS AV295422 304 bp mRNA linear EST 10-NOV-1999
DEFINITION AV295422 RIKEN full-length enriched, 8 days embryo Mus musculus cDNA clone 5730434H04 3' similar to S68987 set=Set beta isoform {alternatively spliced}, mRNA sequence.
ACCESSION AV295422
VERSION AV295422.1 GI:6327439
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 304)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Konno,H., et al. 1999)
JOURNAL Unpublished (1999)
COMMENT Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y., Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES Location/Qualifiers
source 1. .304
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="5730434H04"
/sex="mixed"
/dev_stage="8 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 8 days embryo"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rot = 100.0 Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

ORIGIN

Query Match 90.0%; Score 18; DB 9; Length 304;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAAGGCGAGGATGA 18
||||||||||||||||||
Db 94 GGAGGAAGGCGAGGATGA 111

RESULT 2
BG102240/c
LOCUS BG102240 410 bp mRNA linear EST 30-JAN-2001
DEFINITION RHIZ2_23_H01.b1_A003 Rhizome2 (RHIZ2) Sorghum propinquum cDNA, mRNA sequence.
ACCESSION BG102240
VERSION BG102240.1 GI:12617185
KEYWORDS EST.
SOURCE Sorghum propinquum
ORGANISM Sorghum propinquum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 410)
AUTHORS Cordonnier-Pratt,M.-M., Gingle,A., Paterson,A., Sudman,M. and Pratt,L.H.
TITLE An EST database from Sorghum: Sorghum propinquum rhizomes
JOURNAL Unpublished (2000)
COMMENT Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Seq primer: JEN REV
High quality sequence stop: 377
POLYA=No.

FEATURES Location/Qualifiers
source 1. .410
/organism="Sorghum propinquum"
/mol_type="mRNA"
/db_xref="taxon:132711"
/clone_lib="Rhizome2 (RHIZ2)"
/note="Organ: Rhizomes; Vector: pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."

ORIGIN

Query Match 90.0%; Score 18; DB 12; Length 410;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAAGGCGAGGATGA 18
||||||||||||||||||
Db 251 GGAGGAAGGCGAGGATGA 234

RESULT 3
BG380134/c
LOCUS BG380134 508 bp mRNA linear EST 12-MAR-2001
DEFINITION UI-R-CS0-btp-d-11-0-UI.s1 UI-R-CS0 Rattus norvegicus cDNA clone UI-R-CS0-btp-d-11-0-UI 3', mRNA sequence.
ACCESSION BG380134
VERSION BG380134.1 GI:13304606
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 508)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized rat heart pool library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive

```
          elements were found in this cDNA sequence: 1-23,
          >AT_rich#Low_complexity
          Seq primer: M13 Forward
          POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .508
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-CS0-btp-d-11-0-UI"
                     /dev_stage="ADULT"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="UI-R-CS0"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CS0
                     library is a normalized library constructed from the
                     following rat heart tissues: embryonic day 17, embryonic
                     day 19, embryonic day 21, adult day 1, adult day 12, adult
                     day 75, adult day 200. For a detailed description of the
                     library from which this clone was derived, please visit
                     our web site at ratest.eng.uiowa.edu. The subtraction has
                     been previously described in (Bonaldo, Lennon and Soares,
                     Genome Research 6:791-806, 1996)
                     TAG_TISSUE=rat heart pool
                     TAG_LIB=UI-R-CS0
                     TAG_SEQ=ATAAGATAAC"
ORIGIN

  Query Match             90.0%;  Score 18;  DB 12;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GAGGAAGGCGAGGATGAC 19
              ||||||||||||||||||
Db        349 GAGGAAGGCGAGGATGAC 332


RESULT 4
CG093861
LOCUS       CG093861                530 bp    DNA     linear   GSS 20-AUG-2003
DEFINITION  PUFSX26TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0725F04,
            genomic survey sequence.
ACCESSION   CG093861
VERSION     CG093861.1  GI:33976155
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 530)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUFSX26TD
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .530
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa0725F04"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             90.0%;  Score 18;  DB 29;  Length 530;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGA 18
              ||||||||||||||||||
Db        117 GGAGGAAGGCGAGGATGA 134


RESULT 5
CG093863/c
LOCUS       CG093863                567 bp    DNA     linear   GSS 20-AUG-2003
DEFINITION  PUFSX26TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0725F04,
            genomic survey sequence.
ACCESSION   CG093863
VERSION     CG093863.1  GI:33976157
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 567)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUFSX26TB
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .567
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa0725F04"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             90.0%;  Score 18;  DB 29;  Length 567;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGA 18
              ||||||||||||||||||
Db        415 GGAGGAAGGCGAGGATGA 398


RESULT 6
CA199884/c
LOCUS       CA199884                573 bp    mRNA    linear   EST 25-SEP-2003
DEFINITION  SCRLFL1013D09.g FL1 Saccharum officinarum cDNA clone SCRLFL1013D09
            5', mRNA sequence.
ACCESSION   CA199884
VERSION     CA199884.1  GI:35232591
KEYWORDS    EST.
SOURCE      Saccharum officinarum
  ORGANISM  Saccharum officinarum
```

```
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE   1  (bases 1 to 573)
  AUTHORS   Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
  TITLE     The libraries that made SUCEST
  JOURNAL   Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT     Contact: Arruda P
            Centro de Biologia Molecular e Engenharia Genetica
            Universidade Estadual de Campinas
            Caixa Postal 6010, 13083-970, Campinas SP, Brazil
            Tel: 55 19 3788 1137
            Fax: 55 19 3788 1089
            Email: parruda@unicamp.br
            Clone distribution: clone distribution information can be found
            through the Brazilian Clone Collection Center (BCCC) at
            http://www.bcccenter.fcav.unesp.br
            Plate: 013  row: D  column: 09
            Seq primer: T7 Promoter Primer.
FEATURES              Location/Qualifiers
     source           1. .573
                      /organism="Saccharum officinarum"
                      /mol_type="mRNA"
                      /db_xref="taxon:4547"
                      /clone="SCRLFL1013D09"
                      /lab_host="DH10B"
                      /clone_lib="FL1"
                      /note="Organ: Inflorescence at begining of development
                      (1cm-long); Vector: pSport1; Site_1: SalI; Site_2: NotI;
                      An unidirectional cDNA library generated from
                      [Inflorescence at begining of development (1cm-long)].
                      cDNA was prepared from polyA+ mRNA using SuperScript
                      Plasmid System Kit (Invitrogen). The double-strand cDNAs
                      were fractionated in a sepharose CL-2B 40cm-columns and
                      fragments sizing between 0.8 and 1.5 Kb were
                      directionally cloned into the vector. Details of each
                      source of RNA and library construction can be obtained at
                      http://sucest.lad.ic.unicamp.br/public"
ORIGIN

  Query Match             90.0%;  Score 18;  DB 14;  Length 573;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GAGGAAGGCGAGGATGAC 19
              ||||||||||||||||||
Db        419 GAGGAAGGCGAGGATGAC 402


RESULT 7
CA236557/c
LOCUS       CA236557                617 bp    mRNA    linear   EST 25-SEP-2003
DEFINITION  SCSBFL5014E09.g Saccharum officinarum FL5 Saccharum officinarum
            cDNA clone SCSBFL5014E09 5', mRNA sequence.
ACCESSION   CA236557
VERSION     CA236557.1  GI:35306233
KEYWORDS    EST.
SOURCE      Saccharum officinarum
  ORGANISM  Saccharum officinarum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE   1  (bases 1 to 617)
  AUTHORS   Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
  TITLE     The libraries that made SUCEST
  JOURNAL   Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT     Contact: Arruda P
            Centro de Biologia Molecular e Engenharia Genetica
            Universidade Estadual de Campinas
            Caixa Postal 6010, 13083-970, Campinas SP, Brazil
            Tel: 55 19 3788 1137
            Fax: 55 19 3788 1089
            Email: parruda@unicamp.br
            Clone distribution: clone distribution information can be found
            through the Brazilian Clone Collection Center (BCCC) at
            http://www.bcccenter.fcav.unesp.br
            Plate: 014  row: E  column: 09
            Seq primer: T7 Promoter Primer.
FEATURES              Location/Qualifiers
     source           1. .617
                      /organism="Saccharum officinarum"
                      /mol_type="mRNA"
                      /db_xref="taxon:4547"
                      /clone="SCSBFL5014E09"
                      /lab_host="DH10B"
                      /clone_lib="Saccharum officinarum FL5"
                      /note="Organ: Developed inflorescence (20cm-long) without
                      rachis; Vector: pSport1; Site_1: SalI; Site_2: NotI; An
                      unidirectional cDNA library generated from [Developed
                      inflorescence (20cm-long) without rachis]. cDNA was
                      prepared from polyA+ mRNA using SuperScript Plasmid
                      System Kit (Invitrogen). The double-strand cDNAs were
                      fractionated in a sepharose CL-2B 40cm-columns and
                      fragments sizing between 0.8 and 1.5 Kb were
                      directionally cloned into the vector. Details of each
                      source of RNA and library construction can be obtained at
                      http://sucest.lad.ic.unicamp.br/public"
ORIGIN

  Query Match             90.0%;  Score 18;  DB 14;  Length 617;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGA 18
              ||||||||||||||||||
Db        255 GGAGGAAGGCGAGGATGA 238


RESULT 8
CC657309/c
LOCUS       CC657309                784 bp    DNA     linear   GSS 19-JUN-2003
DEFINITION  OGJAO16TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0295D07,
            genomic survey sequence.
ACCESSION   CC657309
VERSION     CC657309.1  GI:32060634
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 784)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
            Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
  TITLE     Consortium for Maize Genomics
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
FEATURES              Location/Qualifiers
     source           1. .784
                      /organism="Zea mays"
                      /mol_type="genomic DNA"
                      /strain="B73"
                      /db_xref="taxon:4577"
                      /clone="ZMMBMa0295D07"
                      /clone_lib="ZM_0.7_1.5_KB"
                      /note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
                      methylation filtered genomic DNA library"
ORIGIN
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  Query Match             90.0%;  Score 18;  DB 29;  Length 784;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGA 18
              ||||||||||||||||||
Db        484 GGAGGAAGGCGAGGATGA 467


RESULT 9
CG734728/c
LOCUS       CG734728                784 bp    DNA     linear   GSS 22-OCT-2003
DEFINITION  ZMMBBb0290C20.f ZMMBBb Zea mays subsp. mays genomic clone
            ZMMBBb0290C20 5', genomic survey sequence.
ACCESSION   CG734728
VERSION     CG734728.1  GI:37807453
KEYWORDS    GSS.
SOURCE      Zea mays subsp. mays (maize)
  ORGANISM  Zea mays subsp. mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 784)
  AUTHORS   Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.
            and Wing,R.
  TITLE     Sequencing of the maize genome
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Rod Wing
            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: http://genome.arizona.edu
            PCR PRimers
            FORWARD: T7
            BACKWARD: M13r
            Plate: 0290  row: C  column: 20
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .784
                     /organism="Zea mays subsp. mays"
                     /mol_type="genomic DNA"
                     /cultivar="B73"
                     /sub_species="mays"
                     /db_xref="taxon:4578"
                     /clone="ZMMBBb0290C20"
                     /lab_host="DH10B"
                     /clone_lib="ZMMBBb"
                     /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                     HindIII; Zea mays L. ssp. mays"
ORIGIN

  Query Match             90.0%;  Score 18;  DB 29;  Length 784;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGA 18
              ||||||||||||||||||
Db        478 GGAGGAAGGCGAGGATGA 461


RESULT 10
BE743778
LOCUS       BE743778                826 bp    mRNA    linear   EST 15-SEP-2000
DEFINITION  601577886F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926924 5',
            mRNA sequence.
ACCESSION   BE743778
VERSION     BE743778.1  GI:10157770
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 826)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM755  row: k  column: 21
            High quality sequence stop: 771.
FEATURES             Location/Qualifiers
     source          1. .826
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3926924"
                     /tissue_type="adenocarcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_9"
                     /note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

  Query Match             90.0%;  Score 18;  DB 10;  Length 826;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GAGGAAGGCGAGGATGAC 19
              ||||||||||||||||||
Db        598 GAGGAAGGCGAGGATGAC 615


RESULT 11
CG458612
LOCUS       CG458612                867 bp    DNA     linear   GSS 17-SEP-2003
DEFINITION  PUIKZ64TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0607K08,
            genomic survey sequence.
ACCESSION   CG458612
VERSION     CG458612.1  GI:34843612
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 867)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUIKZ64TB
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
```

```
          Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .867
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa0607K08"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             90.0%;  Score 18;  DB 29;  Length 867;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGA 18
              ||||||||||||||||||
Db        405 GGAGGAAGGCGAGGATGA 422


RESULT 12
BZ803618/c
LOCUS       BZ803618                  890 bp    DNA     linear   GSS 17-MAR-2003
DEFINITION  PUFDX67TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa297K14,
            genomic survey sequence.
ACCESSION   BZ803618
VERSION     BZ803618.1  GI:29012224
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 890)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUFDX67TB
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .890
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa297K14"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             90.0%;  Score 18;  DB 28;  Length 890;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGA 18
              ||||||||||||||||||
Db        812 GGAGGAAGGCGAGGATGA 795


RESULT 13
CG038934/c
LOCUS       CG038934                  951 bp    DNA     linear   GSS 19-AUG-2003
DEFINITION  PUFLB28TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0674F08,
            genomic survey sequence.
ACCESSION   CG038934
VERSION     CG038934.1  GI:33911090
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 951)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUFLB28TB
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .951
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
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                     /clone_lib="ZM_0.6_1.0_KB"
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ORIGIN

  Query Match             90.0%;  Score 18;  DB 29;  Length 951;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGA 18
              ||||||||||||||||||
Db        323 GGAGGAAGGCGAGGATGA 306


RESULT 14
CG038933
LOCUS       CG038933                  972 bp    DNA     linear   GSS 19-AUG-2003
DEFINITION  PUFLB28TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0674F08,
            genomic survey sequence.
ACCESSION   CG038933
VERSION     CG038933.1  GI:33911089
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 972)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUFLB28TD
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
```

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           Seq primer: TR
           Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .972
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa0674F08"
                     /clone_lib="ZM_0.6_1.0_KB"
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ORIGIN

  Query Match             90.0%;  Score 18;  DB 29;  Length 972;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGA 18
              ||||||||||||||||||
Db        830 GGAGGAAGGCGAGGATGA 847


RESULT 15
BZ803611
LOCUS       BZ803611               992 bp    DNA     linear   GSS 17-MAR-2003
DEFINITION  PUFDX67TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa297K14,
            genomic survey sequence.
ACCESSION   BZ803611
VERSION     BZ803611.1  GI:29012211
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 992)
  AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
  TITLE     Maize Genomics Consortium
  JOURNAL   Unpublished (2003)
COMMENT     Other_GSSs: PUFDX67TD
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .992
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZMMBTa297K14"
                     /clone_lib="ZM_0.6_1.0_KB"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
                     CoT selected genomic DNA library"
ORIGIN

  Query Match             90.0%;  Score 18;  DB 28;  Length 992;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGA 18
              ||||||||||||||||||
Db        350 GGAGGAAGGCGAGGATGA 367


Search completed: August  4, 2004, 09:20:51
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Job time : 1397.25 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 06:43:54 ; Search time 199.036 Seconds
(without alignments)
247.629 Million cell updates/sec

Title: US-09-940-860-1
Perfect score: 20
Sequence: 1 gcaaacaggattagataccc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4754066 seqs, 1232178907 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9508132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq2:*
8: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq3:*
9: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	20	100.0	279	7	US-10-417-884A-3170	Sequence 3170, Ap
c 2	20	100.0	279	7	US-10-417-884A-3171	Sequence 3171, Ap
3	20	100.0	442	7	US-10-793-479-14013	Sequence 14013, A
4	20	100.0	600	8	US-10-148-328B-74	Sequence 74, Appl
5	20	100.0	601	8	US-10-148-328B-75	Sequence 75, Appl
c 6	20	100.0	755	1	PCT-IL04-00351-5	Sequence 5, Appli
c 7	20	100.0	895	8	US-10-486-307-5	Sequence 5, Appli
8	20	100.0	1113	8	US-10-148-328B-70	Sequence 70, Appl
9	20	100.0	1197	8	US-10-148-328B-100	Sequence 100, App
10	20	100.0	1210	8	US-10-148-328B-81	Sequence 81, Appl
11	20	100.0	1223	8	US-10-148-328B-66	Sequence 66, Appl
12	20	100.0	1225	8	US-10-148-328B-71	Sequence 71, Appl
13	20	100.0	1233	8	US-10-148-328B-98	Sequence 98, Appl
14	20	100.0	1236	8	US-10-148-328B-76	Sequence 76, Appl
15	20	100.0	1237	8	US-10-148-328B-67	Sequence 67, Appl
16	20	100.0	1250	8	US-10-148-328B-92	Sequence 92, Appl
17	20	100.0	1250	8	US-10-148-328B-104	Sequence 104, App
18	20	100.0	1269	8	US-10-148-328B-60	Sequence 60, Appl
19	20	100.0	1276	8	US-10-148-328B-95	Sequence 95, Appl
20	20	100.0	1281	8	US-10-148-328B-106	Sequence 106, App
21	20	100.0	1288	8	US-10-148-328B-64	Sequence 64, Appl
22	20	100.0	1288	8	US-10-148-328B-73	Sequence 73, Appl
23	20	100.0	1292	8	US-10-148-328B-84	Sequence 84, Appl
24	20	100.0	1296	8	US-10-148-328B-91	Sequence 91, Appl
25	20	100.0	1300	8	US-10-148-328B-85	Sequence 85, Appl
26	20	100.0	1307	8	US-10-148-328B-88	Sequence 88, Appl
27	20	100.0	1324	1	PCT-US04-19038-16	Sequence 16, Appl
28	20	100.0	1324	7	US-10-808-807-16	Sequence 16, Appl
29	20	100.0	1327	1	PCT-US04-15524-16	Sequence 16, Appl
30	20	100.0	1327	7	US-10-808-979-16	Sequence 16, Appl
31	20	100.0	1331	1	PCT-US04-13989-16	Sequence 16, Appl
32	20	100.0	1331	7	US-10-804-677-16	Sequence 16, Appl
33	20	100.0	1346	8	US-10-148-328B-68	Sequence 68, Appl
34	20	100.0	1351	1	PCT-US04-22747-18	Sequence 18, Appl
35	20	100.0	1351	7	US-10-810-733-18	Sequence 18, Appl
36	20	100.0	1352	8	US-10-148-328B-101	Sequence 101, App
37	20	100.0	1360	8	US-10-148-328B-63	Sequence 63, Appl
38	20	100.0	1361	8	US-10-148-328B-102	Sequence 102, App
39	20	100.0	1366	8	US-10-148-328B-62	Sequence 62, Appl
40	20	100.0	1382	1	PCT-IL03-00725A-4	Sequence 4, Appli
41	20	100.0	1386	8	US-10-148-328B-65	Sequence 65, Appl
42	20	100.0	1420	8	US-10-875-006-1	Sequence 1, Appli
43	20	100.0	1428	1	PCT-IL03-00725A-3	Sequence 3, Appli
44	20	100.0	1428	7	US-10-727-261-120	Sequence 120, App
45	20	100.0	1429	7	US-10-701-200-81	Sequence 81, Appl

ALIGNMENTS

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RESULT 1
US-10-417-884A-3170/c
; Sequence 3170, Application US/10417884A
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                            ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;        NUMBER OF SEQUENCES: 7310
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;             STREET: 100 Beaver Street
;             CITY: Waltham
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02354
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD/ROM ISO9660
;             COMPUTER: PC
;             OPERATING SYSTEM: <Unknown>
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/417,884A
;             FILING DATE: 17-Apr-2003
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/107,532
;             FILING DATE: 30-Jun-1998
;             APPLICATION NUMBER: 60/085,598
;             FILING DATE: 14 May 1998
;             APPLICATION NUMBER: 60/051571
;             FILING DATE: July 2, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ariniello, Pamela Deneke
;             REGISTRATION NUMBER: 40,489
;             REFERENCE/DOCKET NUMBER: GTC-012
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (781)893-5007
;             TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 3170:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 279 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: circular
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        ORIGINAL SOURCE:
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; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...279
; SEQUENCE DESCRIPTION: SEQ ID NO: 3170:
US-10-417-884A-3170

Query Match 100.0%; Score 20; DB 7; Length 279;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 134 GCAAACAGGATTAGATACCC 115

RESULT 2
US-10-417-884A-3171/c
; Sequence 3171, Application US/10417884A
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/417,884A
; FILING DATE: 17-Apr-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532
; FILING DATE: 30-Jun-1998
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3171:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 279 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...279
; SEQUENCE DESCRIPTION: SEQ ID NO: 3171:
US-10-417-884A-3171

Query Match 100.0%; Score 20; DB 7; Length 279;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 134 GCAAACAGGATTAGATACCC 115

RESULT 3
US-10-793-479-14013
; Sequence 14013, Application US/10793479
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/10/793,479
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US/09/513,999
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 14013
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 363
; OTHER INFORMATION: s=g or c
US-10-793-479-14013

Query Match 100.0%; Score 20; DB 7; Length 442;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 288 GCAAACAGGATTAGATACCC 307

RESULT 4
US-10-148-328B-74
; Sequence 74, Application US/10148328B
; GENERAL INFORMATION:
; APPLICANT: JEANNIN, PASCALE
; APPLICANT: PERNODET, JEAN-LUC
; APPLICANT: GUERINEAU, MICHEL
; APPLICANT: SIMONET, PASCAL
; TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
; TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
; TITLE OF INVENTION: OF NOVEL COMPOUNDS
; FILE REFERENCE: 03806.0547-00000
; CURRENT APPLICATION NUMBER: US/10/148,328B
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: FR9915032
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/FR00/03311
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/209,800
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 74
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Unknown organism
; FEATURE:
; OTHER INFORMATION: Origin of the sequence: soil organism
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (494)

; OTHER INFORMATION: variable nucleotide
US-10-148-328B-74

Query Match 100.0%; Score 20; DB 8; Length 600;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 265 GCAAACAGGATTAGATACCC 284

RESULT 5
US-10-148-328B-75
; Sequence 75, Application US/10148328B
; GENERAL INFORMATION:
; APPLICANT: JEANNIN, PASCALE
; APPLICANT: PERNODET, JEAN-LUC
; APPLICANT: GUERINEAU, MICHEL
; APPLICANT: SIMONET, PASCAL
; TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
; TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
; TITLE OF INVENTION: OF NOVEL COMPOUNDS
; FILE REFERENCE: 03806.0547-00000
; CURRENT APPLICATION NUMBER: US/10/148,328B
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: FR9915032
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/FR00/03311
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/209,800
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 75
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Unknown organism
; FEATURE:
; OTHER INFORMATION: Origin of the sequence: soil organism
US-10-148-328B-75

Query Match 100.0%; Score 20; DB 8; Length 601;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 265 GCAAACAGGATTAGATACCC 284

RESULT 6
PCT-IL04-00351-5/c
; Sequence 5, Application PC/TIL0400351
; GENERAL INFORMATION:
; APPLICANT: Rosenberg, Eugene
; APPLICANT: Ron, Eliora Z.
; APPLICANT: Koren, Omry
; TITLE OF INVENTION: BIOREMEDIATION OF PETROLEUM POLLUTION USING WATER-INSOLUBLE URIC
; TITLE OF INVENTION: ACID AS THE NITROGEN SOURCE
; FILE REFERENCE: 27821
; CURRENT APPLICATION NUMBER: PCT/IL04/00351
; CURRENT FILING DATE: 2004-04-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 755
; TYPE: DNA
; ORGANISM: Acinetobacter sp. strain OK1
PCT-IL04-00351-5

Query Match 100.0%; Score 20; DB 1; Length 755;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 696 GCAAACAGGATTAGATACCC 677

RESULT 7
US-10-486-307-5/c
; Sequence 5, Application US/10486307
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours, Inc.
; TITLE OF INVENTION: GENES ENCODING BAEYER-VILLIGER MONOOXYGENASES
; FILE REFERENCE: CL1789 PCT
; CURRENT APPLICATION NUMBER: US/10/486,307
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: 60/315,546
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 895
; TYPE: DNA
; ORGANISM: Brachymonas sp. CHX
US-10-486-307-5

Query Match 100.0%; Score 20; DB 8; Length 895;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 664 GCAAACAGGATTAGATACCC 645

RESULT 8
US-10-148-328B-70
; Sequence 70, Application US/10148328B
; GENERAL INFORMATION:
; APPLICANT: JEANNIN, PASCALE
; APPLICANT: PERNODET, JEAN-LUC
; APPLICANT: GUERINEAU, MICHEL
; APPLICANT: SIMONET, PASCAL
; TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
; TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
; TITLE OF INVENTION: OF NOVEL COMPOUNDS
; FILE REFERENCE: 03806.0547-00000
; CURRENT APPLICATION NUMBER: US/10/148,328B
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: FR9915032
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/FR00/03311
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/209,800
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 70
; LENGTH: 1113
; TYPE: DNA
; ORGANISM: Unknown organism
; FEATURE:
; OTHER INFORMATION: Origin of the sequence: soil organism
US-10-148-328B-70

Query Match 100.0%; Score 20; DB 8; Length 1113;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 574 GCAAACAGGATTAGATACCC 593

```
RESULT 9
US-10-148-328B-100
; Sequence 100, Application US/10148328B
; GENERAL INFORMATION:
;  APPLICANT: JEANNIN, PASCALE
;  APPLICANT:  PERNODET, JEAN-LUC
;  APPLICANT:  GUERINEAU, MICHEL
;  APPLICANT:  SIMONET, PASCAL
;  TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
;  TITLE OF INVENTION:  SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
;  TITLE OF INVENTION:  OF NOVEL COMPOUNDS
;  FILE REFERENCE: 03806.0547-00000
;  CURRENT APPLICATION NUMBER: US/10/148,328B
;  CURRENT FILING DATE:  2002-05-29
;  PRIOR APPLICATION NUMBER: FR9915032
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/FR00/03311
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/209,800
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 100
;   LENGTH: 1197
;   TYPE: DNA
;   ORGANISM: Unknown organism
;   FEATURE:
;   OTHER INFORMATION: Origin of the sequence: soil organism
US-10-148-328B-100

  Query Match           100.0%;  Score 20;  DB 8;  Length 1197;
  Best Local Similarity  100.0%;  Pred. No. 0.019;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db        642 GCAAACAGGATTAGATACCC 661


RESULT 10
US-10-148-328B-81
; Sequence 81, Application US/10148328B
; GENERAL INFORMATION:
;  APPLICANT: JEANNIN, PASCALE
;  APPLICANT:  PERNODET, JEAN-LUC
;  APPLICANT:  GUERINEAU, MICHEL
;  APPLICANT:  SIMONET, PASCAL
;  TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
;  TITLE OF INVENTION:  SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
;  TITLE OF INVENTION:  OF NOVEL COMPOUNDS
;  FILE REFERENCE: 03806.0547-00000
;  CURRENT APPLICATION NUMBER: US/10/148,328B
;  CURRENT FILING DATE:  2002-05-29
;  PRIOR APPLICATION NUMBER: FR9915032
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/FR00/03311
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/209,800
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 81
;   LENGTH: 1210
;   TYPE: DNA
;   ORGANISM: Unknown organism
;   FEATURE:
;   OTHER INFORMATION: Origin of the sequence: soil organism
US-10-148-328B-81

  Query Match           100.0%;  Score 20;  DB 8;  Length 1210;
  Best Local Similarity  100.0%;  Pred. No. 0.019;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db        616 GCAAACAGGATTAGATACCC 635


RESULT 11
US-10-148-328B-66
; Sequence 66, Application US/10148328B
; GENERAL INFORMATION:
;  APPLICANT: JEANNIN, PASCALE
;  APPLICANT:  PERNODET, JEAN-LUC
;  APPLICANT:  GUERINEAU, MICHEL
;  APPLICANT:  SIMONET, PASCAL
;  TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
;  TITLE OF INVENTION:  SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
;  TITLE OF INVENTION:  OF NOVEL COMPOUNDS
;  FILE REFERENCE: 03806.0547-00000
;  CURRENT APPLICATION NUMBER: US/10/148,328B
;  CURRENT FILING DATE:  2002-05-29
;  PRIOR APPLICATION NUMBER: FR9915032
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/FR00/03311
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/209,800
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 66
;   LENGTH: 1223
;   TYPE: DNA
;   ORGANISM: Unknown organism
;   FEATURE:
;   OTHER INFORMATION: Origin of the sequence: soil organism
US-10-148-328B-66

  Query Match           100.0%;  Score 20;  DB 8;  Length 1223;
  Best Local Similarity  100.0%;  Pred. No. 0.019;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db        638 GCAAACAGGATTAGATACCC 657


RESULT 12
US-10-148-328B-71
; Sequence 71, Application US/10148328B
; GENERAL INFORMATION:
;  APPLICANT: JEANNIN, PASCALE
;  APPLICANT:  PERNODET, JEAN-LUC
;  APPLICANT:  GUERINEAU, MICHEL
;  APPLICANT:  SIMONET, PASCAL
;  TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
;  TITLE OF INVENTION:  SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
;  TITLE OF INVENTION:  OF NOVEL COMPOUNDS
;  FILE REFERENCE: 03806.0547-00000
;  CURRENT APPLICATION NUMBER: US/10/148,328B
;  CURRENT FILING DATE:  2002-05-29
;  PRIOR APPLICATION NUMBER: FR9915032
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/FR00/03311
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/209,800
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 71
;   LENGTH: 1225
;   TYPE: DNA
;   ORGANISM: Unknown organism
;   FEATURE:
;   OTHER INFORMATION: Origin of the sequence: soil organism
```

US-10-148-328B-71

Query Match 100.0%; Score 20; DB 8; Length 1225;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db        641 GCAAACAGGATTAGATACCC 660
```

RESULT 13
US-10-148-328B-98
; Sequence 98, Application US/10148328B
; GENERAL INFORMATION:
; APPLICANT: JEANNIN, PASCALE
; APPLICANT: PERNODET, JEAN-LUC
; APPLICANT: GUERINEAU, MICHEL
; APPLICANT: SIMONET, PASCAL
; TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
; TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
; TITLE OF INVENTION: OF NOVEL COMPOUNDS
; FILE REFERENCE: 03806.0547-00000
; CURRENT APPLICATION NUMBER: US/10/148,328B
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: FR9915032
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/FR00/03311
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/209,800
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 98
; LENGTH: 1233
; TYPE: DNA
; ORGANISM: Unknown organism
; FEATURE:
; OTHER INFORMATION: Origin of the sequence: soil organism
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (435)
; OTHER INFORMATION: variable nucleotide
US-10-148-328B-98

Query Match 100.0%; Score 20; DB 8; Length 1233;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db        644 GCAAACAGGATTAGATACCC 663
```

RESULT 14
US-10-148-328B-76
; Sequence 76, Application US/10148328B
; GENERAL INFORMATION:
; APPLICANT: JEANNIN, PASCALE
; APPLICANT: PERNODET, JEAN-LUC
; APPLICANT: GUERINEAU, MICHEL
; APPLICANT: SIMONET, PASCAL
; TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
; TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
; TITLE OF INVENTION: OF NOVEL COMPOUNDS
; FILE REFERENCE: 03806.0547-00000
; CURRENT APPLICATION NUMBER: US/10/148,328B
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: FR9915032
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/FR00/03311
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/209,800
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 76
; LENGTH: 1236
; TYPE: DNA
; ORGANISM: Unknown organism
; FEATURE:
; OTHER INFORMATION: Origin of the sequence: soil organism
US-10-148-328B-76

Query Match 100.0%; Score 20; DB 8; Length 1236;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db        653 GCAAACAGGATTAGATACCC 672
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RESULT 15
US-10-148-328B-67
; Sequence 67, Application US/10148328B
; GENERAL INFORMATION:
; APPLICANT: JEANNIN, PASCALE
; APPLICANT: PERNODET, JEAN-LUC
; APPLICANT: GUERINEAU, MICHEL
; APPLICANT: SIMONET, PASCAL
; TITLE OF INVENTION: METHOD FOR OBTAINING NUCLEIC ACIDS FROM AN ENVIRONMENT
; TITLE OF INVENTION: SAMPLE, RESULTING NUCLEIC ACIDS AND USE IN SYNTHESIS
; TITLE OF INVENTION: OF NOVEL COMPOUNDS
; FILE REFERENCE: 03806.0547-00000
; CURRENT APPLICATION NUMBER: US/10/148,328B
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: FR9915032
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/FR00/03311
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/209,800
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 67
; LENGTH: 1237
; TYPE: DNA
; ORGANISM: Unknown organism
; FEATURE:
; OTHER INFORMATION: Origin of the sequence: soil organism
US-10-148-328B-67

Query Match 100.0%; Score 20; DB 8; Length 1237;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db        648 GCAAACAGGATTAGATACCC 667
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Search completed: August 4, 2004, 11:43:43
Job time : 200.036 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 06:43:54 ; Search time 199.036 Seconds
(without alignments)
247.629 Million cell updates/sec

Title: US-09-940-860-2
Perfect score: 20
Sequence: 1 ggaggaaggcgaggatgacg 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4754066 seqs, 1232178907 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9508132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_New:*
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8: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq3:*
9: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	18	90.0	850	6	US-10-425-115-28998	Sequence 28998, A
	2	18	90.0	2551	6	US-10-425-115-29000	Sequence 29000, A
c	3	17	85.0	700	6	US-10-425-115-109468	Sequence 109468,
	4	17	85.0	1073	7	US-10-473-974-43	Sequence 43, Appl
	5	17	85.0	1847	7	US-10-767-701-14989	Sequence 14989, A
	6	17	85.0	2097	6	US-10-425-115-151508	Sequence 151508,
	7	16	80.0	352	6	US-10-425-115-130914	Sequence 130914,
c	8	16	80.0	407	7	US-10-767-701-22770	Sequence 22770, A
	9	16	80.0	510	7	US-10-767-701-28210	Sequence 28210, A
	10	16	80.0	551	6	US-10-425-115-38956	Sequence 38956, A
c	11	16	80.0	677	6	US-10-425-115-122047	Sequence 122047,
c	12	16	80.0	788	6	US-10-425-115-126075	Sequence 126075,
c	13	16	80.0	1601	6	US-10-425-115-158496	Sequence 158496,
	14	16	80.0	5536	6	US-10-221-714B-297	Sequence 297, App
c	15	15	75.0	144	7	US-10-674-124A-38	Sequence 38, Appl
c	16	15	75.0	201	9	US-60-582-609-23584	Sequence 23584, A
	17	15	75.0	201	9	US-60-582-609-35417	Sequence 35417, A
	18	15	75.0	285	7	US-10-767-701-30539	Sequence 30539, A
	19	15	75.0	290	7	US-10-430-201-4831	Sequence 4831, Ap
	20	15	75.0	290	7	US-10-430-201-4832	Sequence 4832, Ap
	21	15	75.0	383	6	US-10-425-115-169825	Sequence 169825,
c	22	15	75.0	390	7	US-10-779-543-13155	Sequence 13155, A
	23	15	75.0	400	7	US-10-779-543-12976	Sequence 12976, A
c	24	15	75.0	412	6	US-10-425-115-48631	Sequence 48631, A
c	25	15	75.0	441	6	US-10-425-115-70573	Sequence 70573, A
c	26	15	75.0	454	7	US-10-767-701-22517	Sequence 22517, A
c	27	15	75.0	547	5	US-09-397-206A-4333	Sequence 4333, Ap
c	28	15	75.0	554	6	US-10-425-115-125836	Sequence 125836,
c	29	15	75.0	561	6	US-10-425-115-160109	Sequence 160109,
c	30	15	75.0	697	6	US-10-425-115-98986	Sequence 98986, A
c	31	15	75.0	781	6	US-10-425-115-136893	Sequence 136893,
	32	15	75.0	788	7	US-10-363-345A-26387	Sequence 26387, A
c	33	15	75.0	788	7	US-10-363-345A-26388	Sequence 26388, A
c	34	15	75.0	824	6	US-10-425-115-121769	Sequence 121769,
	35	15	75.0	889	7	US-10-620-246-5	Sequence 5, Appli
c	36	15	75.0	907	6	US-10-425-115-4377	Sequence 4377, Ap
	37	15	75.0	916	7	US-10-363-345A-21759	Sequence 21759, A
c	38	15	75.0	916	7	US-10-363-345A-21760	Sequence 21760, A
	39	15	75.0	927	7	US-10-363-345A-40085	Sequence 40085, A
c	40	15	75.0	927	7	US-10-363-345A-40086	Sequence 40086, A
c	41	15	75.0	976	6	US-10-425-115-103979	Sequence 103979,
c	42	15	75.0	1123	6	US-10-425-115-153306	Sequence 153306,
c	43	15	75.0	1175	7	US-10-767-701-13151	Sequence 13151, A
c	44	15	75.0	1303	6	US-10-425-115-99222	Sequence 99222, A
c	45	15	75.0	1316	7	US-10-767-701-13537	Sequence 13537, A

ALIGNMENTS

RESULT 1
US-10-425-115-28998/c
; Sequence 28998, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 28998
; LENGTH: 850
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(850)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_126457C.1
US-10-425-115-28998

Query Match 90.0%; Score 18; DB 6; Length 850;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAGGAAGGCGAGGATGA 18
              ||||||||||||||||||
Db        617 GGAGGAAGGCGAGGATGA 600
```

RESULT 2
US-10-425-115-29000
; Sequence 29000, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115

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;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 29000
;   LENGTH: 2551
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_126459C.1
US-10-425-115-29000

  Query Match             90.0%;  Score 18;  DB 6;  Length 2551;
  Best Local Similarity   100.0%;  Pred. No. 0.73;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGA 18
              ||||||||||||||||||
Db       1853 GGAGGAAGGCGAGGATGA 1870


RESULT 3
US-10-425-115-109468/c
; Sequence 109468, Application US/10425115
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 109468
;   LENGTH: 700
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_31330C.1
US-10-425-115-109468

  Query Match             85.0%;  Score 17;  DB 6;  Length 700;
  Best Local Similarity   100.0%;  Pred. No. 2.5;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GAGGAAGGCGAGGATGA 18
              |||||||||||||||||
Db        188 GAGGAAGGCGAGGATGA 172


RESULT 4
US-10-473-974-43
; Sequence 43, Application US/10473974
; GENERAL INFORMATION:
;  APPLICANT: GARCIA, TERESA
;  APPLICANT:  ROMAN ROMAN, SERGIO
;  APPLICANT:  BARON, ROLAND
;  APPLICANT:  CALL, KATHERINE
;  APPLICANT:  THEILHABER, JOACHIM
;  APPLICANT:  CONNOLLY, TIMOTHY
;  APPLICANT:  JACKSON, AMANDA
;  APPLICANT:  BUSHNELL, STEVEN
;  APPLICANT:  RAWADI, GEORGES
;  TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
;  FILE REFERENCE: 37991-0023
;  CURRENT APPLICATION NUMBER: US/10/473,974
;  CURRENT FILING DATE:  2003-10-03
;  PRIOR APPLICATION NUMBER: PCT/IB02/02211
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: 60/281,400
;  PRIOR FILING DATE: 2001-04-05
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 43
;   LENGTH: 1073
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-473-974-43

  Query Match             85.0%;  Score 17;  DB 7;  Length 1073;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATG 17
              |||||||||||||||||
Db       1005 GGAGGAAGGCGAGGATG 1021


RESULT 5
US-10-767-701-14989
; Sequence 14989, Application US/10767701
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53535)B
;  CURRENT APPLICATION NUMBER: US/10/767,701
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 14989
;   LENGTH: 1847
;   TYPE: DNA
;   ORGANISM: Sorghum bicolor
;   FEATURE:
;   OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS9317_1
US-10-767-701-14989

  Query Match             85.0%;  Score 17;  DB 7;  Length 1847;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GAGGAAGGCGAGGATGA 18
              |||||||||||||||||
Db       1631 GAGGAAGGCGAGGATGA 1647


RESULT 6
US-10-425-115-151508
; Sequence 151508, Application US/10425115
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 151508
;   LENGTH: 2097
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(2097)
;   OTHER INFORMATION: unsure at all n locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_69698C.1
US-10-425-115-151508

  Query Match             85.0%;  Score 17;  DB 6;  Length 2097;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
```

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 GAGGAAGGCGAGGATGA 18
              |||||||||||||||||
Db       1592 GAGGAAGGCGAGGATGA 1608
```

RESULT 7
US-10-425-115-130914
; Sequence 130914, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 130914
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_50875C.1
US-10-425-115-130914

Query Match 80.0%; Score 16; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          5 GAAGGCGAGGATGACG 20
              ||||||||||||||||
Db        251 GAAGGCGAGGATGACG 266
```

RESULT 8
US-10-767-701-22770/c
; Sequence 22770, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 22770
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 14513702
US-10-767-701-22770

Query Match 80.0%; Score 16; DB 7; Length 407;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 GAGGAAGGCGAGGATG 17
              ||||||||||||||||
Db        167 GAGGAAGGCGAGGATG 152
```

RESULT 9
US-10-767-701-28210
; Sequence 28210, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 28210
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 7535963
US-10-767-701-28210

Query Match 80.0%; Score 16; DB 7; Length 510;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAGGAAGGCGAGGAT 16
              ||||||||||||||||
Db        466 GGAGGAAGGCGAGGAT 481
```

RESULT 10
US-10-425-115-38956
; Sequence 38956, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 38956
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(551)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_135529C.1
US-10-425-115-38956

Query Match 80.0%; Score 16; DB 6; Length 551;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAGGAAGGCGAGGAT 16
              ||||||||||||||||
Db        390 GGAGGAAGGCGAGGAT 405
```

RESULT 11
US-10-425-115-122047/c
; Sequence 122047, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 122047
; LENGTH: 677
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_42791C.1
US-10-425-115-122047

Query Match 80.0%; Score 16; DB 6; Length 677;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GAGGAAGGCGAGGATG 17
||||||||||||||||
Db 415 GAGGAAGGCGAGGATG 400

RESULT 12
US-10-425-115-126075/c
; Sequence 126075, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 126075
; LENGTH: 788
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_4644C.1
US-10-425-115-126075

Query Match 80.0%; Score 16; DB 6; Length 788;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GAAGGCGAGGATGACG 20
||||||||||||||||
Db 254 GAAGGCGAGGATGACG 239

RESULT 13
US-10-425-115-158496/c
; Sequence 158496, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 158496
; LENGTH: 1601
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_76128C.1
US-10-425-115-158496

Query Match 80.0%; Score 16; DB 6; Length 1601;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GAGGAAGGCGAGGATG 17
||||||||||||||||
Db 350 GAGGAAGGCGAGGATG 335

RESULT 14
US-10-221-714B-297
; Sequence 297, Application US/10221714B
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; TITLE OF INVENTION: tumor suppressor genes and oncogenes
; FILE REFERENCE: 5013.1005
; CURRENT APPLICATION NUMBER: US/10/221,714B
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: PCT/EP01/02955
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: DE 10013847.0
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 540
; SEQ ID NO 297
; LENGTH: 5536
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-714B-297

Query Match 80.0%; Score 16; DB 6; Length 5536;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAAGGCGAGGAT 16
||||||||||||||||
Db 1968 GGAGGAAGGCGAGGAT 1983

RESULT 15
US-10-674-124A-38/c
; Sequence 38, Application US/10674124A
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: TAMIYA, Gen
; TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE
; TITLE OF INVENTION: GENETIC POLYMORPHISM MARKERS
; FILE REFERENCE: ORIN-003CIP
; CURRENT APPLICATION NUMBER: US/10/674,124A
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 10/257,511
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/JP00/07621
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: JP2000-112699
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: JP2002-327516
; PRIOR FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: JP2002-383869
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 27110
; SEQ ID NO 38
; LENGTH: 144

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: DIS07_10007639
; FEATURE:
; OTHER INFORMATION: Located on chromosome 1
; FEATURE:
; OTHER INFORMATION: Distance between a terminus base of telomere on
; OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base
; OTHER INFORMATION: sequence : 5692908
; FEATURE:
; OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
; OTHER INFORMATION: sequence listing upward to telomere on chrosomal short arm and
; OTHER INFORMATION: 5'-terminus of this base sequence : 168636
US-10-674-124A-38

Query Match 75.0%; Score 15; DB 7; Length 144;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAGGAAGGCGAGGA 15
              |||||||||||||||
Db         28 GGAGGAAGGCGAGGA 14
```

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Job time : 200.036 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 07:44:29 ; Search time 180.964 Seconds
(without alignments)
541.892 Million cell updates/sec

Title: US-09-940-860-1
Perfect score: 20
Sequence: 1 gcaaacaggattagataccc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3222919 seqs, 2451570024 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	11	US-09-940-860-1	Sequence 1, Appli
	2	20	100.0	25	17	US-10-715-220-1	Sequence 1, Appli
	3	20	100.0	30	11	US-09-940-860-6	Sequence 6, Appli
	4	20	100.0	50	12	US-10-343-319-76	Sequence 76, Appl
	5	20	100.0	50	12	US-10-343-319-77	Sequence 77, Appl
	6	20	100.0	50	12	US-10-343-319-79	Sequence 79, Appl
	7	20	100.0	50	12	US-10-343-319-80	Sequence 80, Appl
	8	20	100.0	50	12	US-10-343-319-81	Sequence 81, Appl
	9	20	100.0	50	12	US-10-343-319-82	Sequence 82, Appl
	10	20	100.0	50	12	US-10-343-319-83	Sequence 83, Appl
	11	20	100.0	50	12	US-10-343-319-84	Sequence 84, Appl
	12	20	100.0	50	12	US-10-343-319-85	Sequence 85, Appl
	13	20	100.0	50	12	US-10-343-319-87	Sequence 87, Appl
	14	20	100.0	50	12	US-10-343-319-88	Sequence 88, Appl
	15	20	100.0	50	12	US-10-343-319-89	Sequence 89, Appl
	16	20	100.0	50	12	US-10-343-319-90	Sequence 90, Appl
	17	20	100.0	50	12	US-10-343-319-91	Sequence 91, Appl
	18	20	100.0	50	12	US-10-343-319-98	Sequence 98, Appl
	19	20	100.0	50	12	US-10-343-319-99	Sequence 99, Appl
	20	20	100.0	50	12	US-10-343-319-102	Sequence 102, App
	21	20	100.0	50	12	US-10-343-319-104	Sequence 104, App
	22	20	100.0	50	12	US-10-343-319-105	Sequence 105, App
	23	20	100.0	293	17	US-10-410-040A-19	Sequence 19, Appl
	24	20	100.0	294	17	US-10-410-040A-15	Sequence 15, Appl
	25	20	100.0	294	17	US-10-410-040A-16	Sequence 16, Appl
	26	20	100.0	294	17	US-10-410-040A-17	Sequence 17, Appl
	27	20	100.0	294	17	US-10-410-040A-18	Sequence 18, Appl
	28	20	100.0	294	17	US-10-410-040A-20	Sequence 20, Appl
	29	20	100.0	294	17	US-10-410-040A-21	Sequence 21, Appl
	30	20	100.0	294	17	US-10-410-040A-23	Sequence 23, Appl
	31	20	100.0	549	10	US-09-991-936-1717	Sequence 1717, Ap
	32	20	100.0	571	9	US-09-879-536-755	Sequence 755, App
c	33	20	100.0	624	9	US-09-879-536-728	Sequence 728, App
	34	20	100.0	665	9	US-09-879-536-476	Sequence 476, App
	35	20	100.0	672	9	US-09-879-536-450	Sequence 450, App
	36	20	100.0	856	15	US-10-213-878-5	Sequence 5, Appli
	37	20	100.0	856	15	US-10-214-059-5	Sequence 5, Appli
c	38	20	100.0	895	15	US-10-230-026-5	Sequence 5, Appli
	39	20	100.0	1009	9	US-09-900-876-1	Sequence 1, Appli
	40	20	100.0	1070	9	US-09-737-297-2	Sequence 2, Appli
	41	20	100.0	1140	9	US-09-737-297-5	Sequence 5, Appli
	42	20	100.0	1208	9	US-09-894-467-1	Sequence 1, Appli
	43	20	100.0	1320	15	US-10-168-337A-7	Sequence 7, Appli
	44	20	100.0	1322	15	US-10-168-337A-5	Sequence 5, Appli
	45	20	100.0	1335	15	US-10-029-397A-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-09-940-860-1
; Sequence 1, Application US/09940860
; Publication No. US20040005555A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, Richard
; APPLICANT: Majmudar, Maulik
; TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
; FILE REFERENCE: 01107.00185
; CURRENT APPLICATION NUMBER: US/09/940,860
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/229,376
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic amplification primer
US-09-940-860-1

Query Match 100.0%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 1 GCAAACAGGATTAGATACCC 20

RESULT 2
US-10-715-220-1
; Sequence 1, Application US/10715220
; Publication No. US20040077015A1
; GENERAL INFORMATION:

; APPLICANT: Vojdani, A.
; TITLE OF INVENTION: DETECTION OF MYCOPLASMA IN PATIENTS WITH
; TITLE OF INVENTION: CHRONIC FATIGUE SYNDROME AND RELATED DISORDERS
; FILE REFERENCE: IMSCI.009A
; CURRENT APPLICATION NUMBER: US/10/715,220
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: US/09/283,655
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide primer
US-10-715-220-1

Query Match 100.0%; Score 20; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 5 GCAAACAGGATTAGATACCC 24

RESULT 3
US-09-940-860-6
; Sequence 6, Application US/09940860
; Publication No. US20040005555A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, Richard
; APPLICANT: Majmudar, Maulik
; TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
; FILE REFERENCE: 01107.00185
; CURRENT APPLICATION NUMBER: US/09/940,860
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/229,376
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic amplification primer
US-09-940-860-6

Query Match 100.0%; Score 20; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 2 GCAAACAGGATTAGATACCC 21

RESULT 4
US-10-343-319-76
; Sequence 76, Application US/10343319
; Publication No. US20040072242A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjelda E.
; APPLICANT: Nardkani, Mangala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: AU PQ9090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Campylobacter jejuni
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Helicobacter pylori also.
US-10-343-319-76

Query Match 100.0%; Score 20; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 16 GCAAACAGGATTAGATACCC 35

RESULT 5
US-10-343-319-77
; Sequence 77, Application US/10343319
; Publication No. US20040072242A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjelda E.
; APPLICANT: Nardkani, Mangala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: AU PQ9090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 77
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Treponema denticola
US-10-343-319-77

Query Match 100.0%; Score 20; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 16 GCAAACAGGATTAGATACCC 35

RESULT 6
US-10-343-319-79
; Sequence 79, Application US/10343319
; Publication No. US20040072242A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjelda E.
; APPLICANT: Nardkani, Mangala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27

```
;  PRIOR APPLICATION NUMBER: AU PQ9090/2000
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 79
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Leptothrix mobilis
US-10-343-319-79

  Query Match           100.0%;  Score 20;  DB 12;  Length 50;
  Best Local Similarity  100.0%;  Pred. No. 0.024;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         16 GCAAACAGGATTAGATACCC 35


RESULT 7
US-10-343-319-80
; Sequence 80, Application US/10343319
; Publication No. US20040072242A1
; GENERAL INFORMATION:
;  APPLICANT: Hunter, Neil
;  APPLICANT:  Jacques, Nicholas A.
;  APPLICANT:  Martin, Fjelda E.
;  APPLICANT:  Nardkani, Mangala A.
;  TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
;  FILE REFERENCE: DAVI139.002APC
;  CURRENT APPLICATION NUMBER: US/10/343,319
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: PCT/AU01/00933
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: AU PQ9090/2000
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 80
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Thiomicrospira denitrificans
US-10-343-319-80

  Query Match           100.0%;  Score 20;  DB 12;  Length 50;
  Best Local Similarity  100.0%;  Pred. No. 0.024;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         16 GCAAACAGGATTAGATACCC 35


RESULT 8
US-10-343-319-81
; Sequence 81, Application US/10343319
; Publication No. US20040072242A1
; GENERAL INFORMATION:
;  APPLICANT: Hunter, Neil
;  APPLICANT:  Jacques, Nicholas A.
;  APPLICANT:  Martin, Fjelda E.
;  APPLICANT:  Nardkani, Mangala A.
;  TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
;  FILE REFERENCE: DAVI139.002APC
;  CURRENT APPLICATION NUMBER: US/10/343,319
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: PCT/AU01/00933
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: AU PQ9090/2000
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 81
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Neisseria meningitidis
US-10-343-319-81

  Query Match           100.0%;  Score 20;  DB 12;  Length 50;
  Best Local Similarity  100.0%;  Pred. No. 0.024;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         16 GCAAACAGGATTAGATACCC 35


RESULT 9
US-10-343-319-82
; Sequence 82, Application US/10343319
; Publication No. US20040072242A1
; GENERAL INFORMATION:
;  APPLICANT: Hunter, Neil
;  APPLICANT:  Jacques, Nicholas A.
;  APPLICANT:  Martin, Fjelda E.
;  APPLICANT:  Nardkani, Mangala A.
;  TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
;  FILE REFERENCE: DAVI139.002APC
;  CURRENT APPLICATION NUMBER: US/10/343,319
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: PCT/AU01/00933
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: AU PQ9090/2000
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 82
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Actinobacillus actinomycetemcomitans
US-10-343-319-82

  Query Match           100.0%;  Score 20;  DB 12;  Length 50;
  Best Local Similarity  100.0%;  Pred. No. 0.024;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         16 GCAAACAGGATTAGATACCC 35


RESULT 10
US-10-343-319-83
; Sequence 83, Application US/10343319
; Publication No. US20040072242A1
; GENERAL INFORMATION:
;  APPLICANT: Hunter, Neil
;  APPLICANT:  Jacques, Nicholas A.
;  APPLICANT:  Martin, Fjelda E.
;  APPLICANT:  Nardkani, Mangala A.
;  TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
;  FILE REFERENCE: DAVI139.002APC
;  CURRENT APPLICATION NUMBER: US/10/343,319
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: PCT/AU01/00933
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: AU PQ9090/2000
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 83
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Haemophilus influenzae
US-10-343-319-83
```

Query Match 100.0%; Score 20; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         16 GCAAACAGGATTAGATACCC 35
```

RESULT 11
US-10-343-319-84
; Sequence 84, Application US/10343319
; Publication No. US20040072242A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjelda E.
; APPLICANT: Nardkani, Mangala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: AU PQ9090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-343-319-84

Query Match 100.0%; Score 20; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         16 GCAAACAGGATTAGATACCC 35
```

RESULT 12
US-10-343-319-85
; Sequence 85, Application US/10343319
; Publication No. US20040072242A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjelda E.
; APPLICANT: Nardkani, Mangala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: AU PQ9090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Salmonella typhi
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Also Vibrio cholerae, Pseudomonas aeruginosa, and
; OTHER INFORMATION: Rhodospirillum rubrum.
US-10-343-319-85

Query Match 100.0%; Score 20; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         16 GCAAACAGGATTAGATACCC 35
```

RESULT 13
US-10-343-319-87
; Sequence 87, Application US/10343319
; Publication No. US20040072242A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjelda E.
; APPLICANT: Nardkani, Mangala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: AU PQ9090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Legionella pneumophila
US-10-343-319-87

Query Match 100.0%; Score 20; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         16 GCAAACAGGATTAGATACCC 35
```

RESULT 14
US-10-343-319-88
; Sequence 88, Application US/10343319
; Publication No. US20040072242A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, Neil
; APPLICANT: Jacques, Nicholas A.
; APPLICANT: Martin, Fjelda E.
; APPLICANT: Nardkani, Mangala A.
; TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
; FILE REFERENCE: DAVI139.002APC
; CURRENT APPLICATION NUMBER: US/10/343,319
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/AU01/00933
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: AU PQ9090/2000
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Caulobacter vibrioides
US-10-343-319-88

Query Match 100.0%; Score 20; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GCAAACAGGATTAGATACCC 20
```

```
                    ||||||||||||||||||||
Db         16 GCAAACAGGATTAGATACCC 35


RESULT 15
US-10-343-319-89
; Sequence 89, Application US/10343319
; Publication No. US20040072242A1
; GENERAL INFORMATION:
;  APPLICANT: Hunter, Neil
;  APPLICANT:  Jacques, Nicholas A.
;  APPLICANT:  Martin, Fjelda E.
;  APPLICANT:  Nardkani, Mangala A.
;  TITLE OF INVENTION: A METHOD OF DETECTING MICROORGANISMS
;  FILE REFERENCE: DAVI139.002APC
;  CURRENT APPLICATION NUMBER: US/10/343,319
;  CURRENT FILING DATE:  2003-09-17
;  PRIOR APPLICATION NUMBER: PCT/AU01/00933
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: AU PQ9090/2000
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 89
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: Nitrobacter winogradskyi
US-10-343-319-89

  Query Match            100.0%;  Score 20;  DB 12;  Length 50;
  Best Local Similarity  100.0%;  Pred. No. 0.024;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
                ||||||||||||||||||||
Db         16 GCAAACAGGATTAGATACCC 35


Search completed: August  4, 2004, 11:56:21
Job time : 180.964 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 07:44:29 ; Search time 180.964 Seconds
(without alignments)
541.892 Million cell updates/sec

Title: US-09-940-860-2
Perfect score: 20
Sequence: 1 ggaggaaggcgaggatgacg 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3222919 seqs, 2451570024 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	11	US-09-940-860-2	Sequence 2, Appli
2	20	100.0	30	11	US-09-940-860-7	Sequence 7, Appli
3	20	100.0	1548	9	US-09-726-774-11	Sequence 11, Appl
4	20	100.0	1548	17	US-10-719-633-11	Sequence 11, Appl
5	20	100.0	1550	11	US-09-940-860-5	Sequence 5, Appli
6	20	100.0	1230025	16	US-10-289-762-1	Sequence 1, Appli
c 7	18	90.0	2123	13	US-10-425-114-4575	Sequence 4575, Ap
c 8	18	90.0	2738	17	US-10-437-963-25445	Sequence 25445, A
9	17	85.0	1143	17	US-10-437-963-4673	Sequence 4673, Ap
10	17	85.0	1305	13	US-10-425-114-32946	Sequence 32946, A
c 11	17	85.0	2124	13	US-10-425-114-32781	Sequence 32781, A
c 12	17	85.0	2145	16	US-10-369-493-35514	Sequence 35514, A
13	16	80.0	338	13	US-10-425-114-25403	Sequence 25403, A
14	16	80.0	1251	13	US-10-282-122A-17957	Sequence 17957, A
c 15	16	80.0	1543	13	US-10-425-114-15476	Sequence 15476, A
c 16	16	80.0	1554	13	US-10-425-114-3138	Sequence 3138, Ap
c 17	16	80.0	1594	13	US-10-425-114-15935	Sequence 15935, A
18	16	80.0	3962	17	US-10-437-963-72402	Sequence 72402, A
19	16	80.0	5536	13	US-10-221-714A-297	Sequence 297, App
20	16	80.0	5536	15	US-10-311-455-1805	Sequence 1805, Ap
21	15	75.0	168	17	US-10-437-963-26084	Sequence 26084, A
c 22	15	75.0	178	9	US-09-923-876-5759	Sequence 5759, Ap
c 23	15	75.0	178	11	US-09-923-876-5759	Sequence 5759, Ap
c 24	15	75.0	236	12	US-09-922-293-666	Sequence 666, App
c 25	15	75.0	254	12	US-09-922-293-989	Sequence 989, App
c 26	15	75.0	266	12	US-09-922-293-504	Sequence 504, App
c 27	15	75.0	274	12	US-09-922-293-509	Sequence 509, App
c 28	15	75.0	281	9	US-09-294-093B-873	Sequence 873, App
c 29	15	75.0	281	12	US-09-922-293-506	Sequence 506, App
c 30	15	75.0	293	12	US-09-922-293-508	Sequence 508, App
c 31	15	75.0	294	9	US-09-294-093B-5844	Sequence 5844, Ap
32	15	75.0	313	17	US-10-437-963-67279	Sequence 67279, A
33	15	75.0	318	17	US-10-437-963-68928	Sequence 68928, A
c 34	15	75.0	320	12	US-09-922-293-503	Sequence 503, App
c 35	15	75.0	357	9	US-09-770-791-589	Sequence 589, App
36	15	75.0	405	9	US-09-867-701-4895	Sequence 4895, Ap
c 37	15	75.0	421	10	US-09-814-353-14381	Sequence 14381, A
c 38	15	75.0	455	10	US-09-814-353-1641	Sequence 1641, Ap
c 39	15	75.0	455	10	US-09-814-353-7997	Sequence 7997, Ap
c 40	15	75.0	499	13	US-10-342-887-2152	Sequence 2152, Ap
c 41	15	75.0	499	13	US-10-172-118-2152	Sequence 2152, Ap
42	15	75.0	525	9	US-09-938-842A-2377	Sequence 2377, Ap
43	15	75.0	525	11	US-09-938-842A-2377	Sequence 2377, Ap
44	15	75.0	543	17	US-10-437-963-4676	Sequence 4676, Ap
c 45	15	75.0	585	13	US-10-027-632-236613	Sequence 236613,

ALIGNMENTS

RESULT 1
US-09-940-860-2
; Sequence 2, Application US/09940860
; Publication No. US20040005555A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, Richard
; APPLICANT: Majmudar, Maulik
; TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
; FILE REFERENCE: 01107.00185
; CURRENT APPLICATION NUMBER: US/09/940,860
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/229,376
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic amplification primer
US-09-940-860-2

Query Match 100.0%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAAGGCGAGGATGACG 20
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Db 1 GGAGGAAGGCGAGGATGACG 20

RESULT 2
US-09-940-860-7
; Sequence 7, Application US/09940860
; Publication No. US20040005555A1
; GENERAL INFORMATION:

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;  APPLICANT: Rothman, Richard
;  APPLICANT:  Majmudar, Maulik
;  TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
;  FILE REFERENCE: 01107.00185
;  CURRENT APPLICATION NUMBER: US/09/940,860
;  CURRENT FILING DATE:  2001-08-29
;  PRIOR APPLICATION NUMBER: 60/229,376
;  PRIOR FILING DATE: 2000-08-31
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic amplification primer
US-09-940-860-7

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  Best Local Similarity   100.0%;  Pred. No. 0.094;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
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Db          3 GGAGGAAGGCGAGGATGACG 22


RESULT 3
US-09-726-774-11
; Sequence 11, Application US/09726774
; Patent No. US20020082226A1
; GENERAL INFORMATION:
;  APPLICANT: Iversen, Patrick L.
;  TITLE OF INVENTION: Antisense Antibacterial Method and
;  TITLE OF INVENTION:  Composition
;  FILE REFERENCE: 0450-0032.30
;  CURRENT APPLICATION NUMBER: US/09/726,774
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER: US 60/168,150
;  PRIOR FILING DATE: 1999-11-29
;  NUMBER OF SEQ ID NOS: 139
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 1548
;   TYPE: DNA
;   ORGANISM: Chlamydia trachomatis
US-09-726-774-11

  Query Match             100.0%;  Score 20;  DB 9;  Length 1548;
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
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Db       1179 GGAGGAAGGCGAGGATGACG 1198


RESULT 4
US-10-719-633-11
; Sequence 11, Application US/10719633
; Publication No. US20040137485A1
; GENERAL INFORMATION:
;  APPLICANT: Iversen, Patrick L.
;  TITLE OF INVENTION: Antisense Antibacterial Method and
;  TITLE OF INVENTION:  Composition
;  FILE REFERENCE: 0450-0032.30
;  CURRENT APPLICATION NUMBER: US/10/719,633
;  CURRENT FILING DATE:  2003-11-21
;  PRIOR APPLICATION NUMBER: US/09/726,774
;  PRIOR FILING DATE: 2000-11-29
;  PRIOR APPLICATION NUMBER: US 60/168,150
;  PRIOR FILING DATE: 1999-11-29
;  NUMBER OF SEQ ID NOS: 139
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 1548
;   TYPE: DNA
;   ORGANISM: Chlamydia trachomatis
US-10-719-633-11

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  Best Local Similarity   100.0%;  Pred. No. 0.049;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
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Db       1179 GGAGGAAGGCGAGGATGACG 1198


RESULT 5
US-09-940-860-5
; Sequence 5, Application US/09940860
; Publication No. US20040005555A1
; GENERAL INFORMATION:
;  APPLICANT: Rothman, Richard
;  APPLICANT:  Majmudar, Maulik
;  TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
;  FILE REFERENCE: 01107.00185
;  CURRENT APPLICATION NUMBER: US/09/940,860
;  CURRENT FILING DATE:  2001-08-29
;  PRIOR APPLICATION NUMBER: 60/229,376
;  PRIOR FILING DATE: 2000-08-31
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 1550
;   TYPE: DNA
;   ORGANISM: Chlamydia trichomatis
US-09-940-860-5

  Query Match             100.0%;  Score 20;  DB 11;  Length 1550;
  Best Local Similarity   100.0%;  Pred. No. 0.049;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
              ||||||||||||||||||||
Db       1179 GGAGGAAGGCGAGGATGACG 1198


RESULT 6
US-10-289-762-1
; Sequence 1, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
;   LENGTH: 1230025
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
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;   NAME/KEY: misc_feature
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;   NAME/KEY: misc_feature
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;   NAME/KEY: misc_feature
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;   LOCATION: (255001)..(270000)
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;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (285001)..(300000)
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;   LOCATION: (315001)..(330000)
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;   NAME/KEY: misc_feature
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;   LOCATION: (435001)..(450000)
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;   FEATURE:
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;   LOCATION: (450001)..(465000)
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;   FEATURE:
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;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (480001)..(495000)
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;   LOCATION: (495001)..(510000)
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;   LOCATION: (510001)..(525000)
;   OTHER INFORMATION: n=a or c or g or t
;   FEATURE:
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;   LOCATION: (525001)..(540000)
;   OTHER INFORMATION: n=a or c or g or t
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;   LOCATION: (540001)..(555000)
;   OTHER INFORMATION: n=a or c or g or t
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;   NAME/KEY: misc_feature
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;   OTHER INFORMATION: n=a or c or g or t
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;   FEATURE:
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;   LOCATION: (615001)..(630000)
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;   LOCATION: (630001)..(645000)
;   OTHER INFORMATION: n=a or c or g or t
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;   LOCATION: (645001)..(660000)
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;   NAME/KEY: misc_feature
;   LOCATION: (660001)..(675000)
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  Query Match            100.0%;  Score 20;  DB 16;  Length 1230025;
  Best Local Similarity  100.0%;  Pred. No. 0.016;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
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Db    1011866 GGAGGAAGGCGAGGATGACG 1011885


RESULT 7
US-10-425-114-4575/c
; Sequence 4575, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 4575
;   LENGTH: 2123
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 700382382_FLI
US-10-425-114-4575

  Query Match            90.0%;  Score 18;  DB 13;  Length 2123;
  Best Local Similarity  100.0%;  Pred. No. 0.61;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGA 18
              ||||||||||||||||||
Db        305 GGAGGAAGGCGAGGATGA 288


RESULT 8
US-10-437-963-25445/c
; Sequence 25445, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Wu, Wei
;  APPLICANT:  Boukharov, Andrey A.
;  APPLICANT:  Barbazuk, Brad
;  APPLICANT:  Li, Ping
;  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53221)B
;  CURRENT APPLICATION NUMBER: US/10/437,963
;  CURRENT FILING DATE:  2003-05-14
;  NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 25445
;   LENGTH: 2738
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_30330C.1
US-10-437-963-25445

  Query Match            90.0%;  Score 18;  DB 17;  Length 2738;
  Best Local Similarity  100.0%;  Pred. No. 0.59;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGA 18
              ||||||||||||||||||
Db        614 GGAGGAAGGCGAGGATGA 597


RESULT 9
US-10-437-963-4673
; Sequence 4673, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Wu, Wei
;  APPLICANT:  Boukharov, Andrey A.
;  APPLICANT:  Barbazuk, Brad
;  APPLICANT:  Li, Ping
;  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53221)B
;  CURRENT APPLICATION NUMBER: US/10/437,963
;  CURRENT FILING DATE:  2003-05-14
;  NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 4673
;   LENGTH: 1143
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_11535C.1
US-10-437-963-4673

  Query Match            85.0%;  Score 17;  DB 17;  Length 1143;
  Best Local Similarity  100.0%;  Pred. No. 2.4;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATG 17
              |||||||||||||||||
Db        816 GGAGGAAGGCGAGGATG 832


RESULT 10
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US-10-425-114-32946
; Sequence 32946, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
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;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: UC-ZMFLMO17043F07_FLI
US-10-425-114-32946

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Db       1122 GAGGAAGGCGAGGATGA 1138


RESULT 11
US-10-425-114-32781/c
; Sequence 32781, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 32781
;   LENGTH: 2124
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: UC-ZMFLMO17021D09_FLI
US-10-425-114-32781

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Db        190 GAGGAAGGCGAGGATGA 174


RESULT 12
US-10-369-493-35514/c
; Sequence 35514, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
;  APPLICANT: Cao, Yongwei
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Goldman, Barry S.
;  APPLICANT:  Chen, Xianfeng
;  TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
;  TITLE OF INVENTION:  PLANTS WITH IMPROVED PROPERTIES
;  FILE REFERENCE: 38-10(52052)B
;  CURRENT APPLICATION NUMBER: US/10/369,493
;  CURRENT FILING DATE:  2003-02-28
;  PRIOR APPLICATION NUMBER: US 60/360,039
;  PRIOR FILING DATE: 2002-02-21
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US-10-369-493-35514

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RESULT 13
US-10-425-114-25403
; Sequence 25403, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
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;   FEATURE:
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RESULT 14
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; Sequence 17957, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT:  Zamudio, Carlos
;  APPLICANT:  Malone, Cheryl
;  APPLICANT:  Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari
;  APPLICANT:  Zyskind, Judith
;  APPLICANT:  Wall, Daniel
```

; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
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; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
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; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
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; LENGTH: 1251
; TYPE: DNA
; ORGANISM: Cornyebacterium diptheriae
US-10-282-122A-17957

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Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 403 GAGGAAGGCGAGGATG 418

RESULT 15
US-10-425-114-15476/c
; Sequence 15476, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
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; LENGTH: 1543
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3060-007-A11_FLI
US-10-425-114-15476

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Best Local Similarity 100.0%; Pred. No. 8.4;
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GenCore version 5.1.6

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	20	100.0	1548	54	US-10-719-633-11	Sequence 11, Appl
4	20	100.0	1550	39	US-09-940-860-5	Sequence 5, Appli
c 5	20	100.0	1038608	16	US-09-201-228A-1	Sequence 1, Appli
6	20	100.0	1230025	48	US-10-289-762-1	Sequence 1, Appli
7	20	100.0	1230230	20	US-09-438-185-1	Sequence 1, Appli
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c 9	18	90.0	2123	47	US-10-219-999-18302	Sequence 18302, A
c 10	18	90.0	2123	51	US-10-425-114-4575	Sequence 4575, Ap
c 11	18	90.0	2123	51	US-10-425-114A-4575	Sequence 4575, Ap
c 12	18	90.0	2738	51	US-10-437-963-25445	Sequence 25445, A
c 13	18	90.0	13218	30	US-09-702-134-21825	Sequence 21825, A
c 14	18	90.0	13218	33	US-09-815-264-71774	Sequence 71774, A
c 15	18	90.0	13263	26	US-09-620-392-33867	Sequence 33867, A
c 16	17	85.0	231	16	US-09-236-218A-1587	Sequence 1587, Ap
c 17	17	85.0	231	40	US-09-955-568-1587	Sequence 1587, Ap
c 18	17	85.0	245	17	US-09-293-979A-2609	Sequence 2609, Ap
c 19	17	85.0	245	42	US-09-982-402-2609	Sequence 2609, Ap
c 20	17	85.0	245	64	US-60-085-146-2609	Sequence 2609, Ap
c 21	17	85.0	309	17	US-09-280-918A-696	Sequence 696, App
c 22	17	85.0	309	63	US-60-079-469-696	Sequence 696, App
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c 24	17	85.0	313	76	US-60-209-830-12489	Sequence 12489, A
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c 26	17	85.0	410	76	US-60-207-458-3288	Sequence 3288, Ap
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c 28	17	85.0	415	76	US-60-202-214-17594	Sequence 17594, A
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c 32	17	85.0	440	34	US-09-849-526A-27635	Sequence 27635, A
c 33	17	85.0	440	76	US-60-202-214-27390	Sequence 27390, A
c 34	17	85.0	443	35	US-09-865-439A-49839	Sequence 49839, A
c 35	17	85.0	443	76	US-60-207-458-94095	Sequence 94095, A
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c 38	17	85.0	458	27	US-09-654-617-272567	Sequence 272567,
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ALIGNMENTS

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; GENERAL INFORMATION:
;  APPLICANT: Rothman, Richard
;  APPLICANT:  Majmudar, Maulik
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;  FILE REFERENCE: 01107.00185
;  CURRENT APPLICATION NUMBER: US/09/940,860
;  CURRENT FILING DATE:  2001-08-29
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;  PRIOR FILING DATE: 2000-08-31
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;   OTHER INFORMATION: synthetic amplification primer
US-09-940-860-2

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US-09-940-860-7
; Sequence 7, Application US/09940860
; GENERAL INFORMATION:
;  APPLICANT: Rothman, Richard
;  APPLICANT:  Majmudar, Maulik
;  TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
;  FILE REFERENCE: 01107.00185
;  CURRENT APPLICATION NUMBER: US/09/940,860
;  CURRENT FILING DATE:  2001-08-29
;  PRIOR APPLICATION NUMBER: 60/229,376
;  PRIOR FILING DATE: 2000-08-31
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 30
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic amplification primer
US-09-940-860-7

  Query Match             100.0%;  Score 20;  DB 39;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.9;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
              ||||||||||||||||||||
Db          3 GGAGGAAGGCGAGGATGACG 22


RESULT 3
US-10-719-633-11
; Sequence 11, Application US/10719633
; GENERAL INFORMATION:
;  APPLICANT: Iversen, Patrick L.
;  TITLE OF INVENTION: Antisense Antibacterial Method and
;  TITLE OF INVENTION:  Composition
;  FILE REFERENCE: 0450-0032.30
;  CURRENT APPLICATION NUMBER: US/10/719,633
;  CURRENT FILING DATE:  2003-11-21
;  PRIOR APPLICATION NUMBER: US/09/726,774
;  PRIOR FILING DATE: 2000-11-29
;  PRIOR APPLICATION NUMBER: US 60/168,150
;  PRIOR FILING DATE: 1999-11-29
;  NUMBER OF SEQ ID NOS: 139
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 1548
;   TYPE: DNA
;   ORGANISM: Chlamydia trachomatis
US-10-719-633-11

  Query Match             100.0%;  Score 20;  DB 54;  Length 1548;
  Best Local Similarity   100.0%;  Pred. No. 1.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
              ||||||||||||||||||||
Db       1179 GGAGGAAGGCGAGGATGACG 1198
```

```
RESULT 4
US-09-940-860-5
; Sequence 5, Application US/09940860
; GENERAL INFORMATION:
;  APPLICANT: Rothman, Richard
;  APPLICANT:  Majmudar, Maulik
;  TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF BACTEREMIA
;  FILE REFERENCE: 01107.00185
;  CURRENT APPLICATION NUMBER: US/09/940,860
;  CURRENT FILING DATE:  2001-08-29
;  PRIOR APPLICATION NUMBER: 60/229,376
;  PRIOR FILING DATE: 2000-08-31
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 1550
;   TYPE: DNA
;   ORGANISM: Chlamydia trichomatis
US-09-940-860-5

  Query Match             100.0%;  Score 20;  DB 39;  Length 1550;
  Best Local Similarity   100.0%;  Pred. No. 1.6;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
              ||||||||||||||||||||
Db       1179 GGAGGAAGGCGAGGATGACG 1198


RESULT 5
US-09-201-228A-1/c
; Sequence 1, Application US/09201228A
; GENERAL INFORMATION:
;  APPLICANT:  Griffais, Remy
;  APPLICANT:  Hoiseth, Susan K.
;  APPLICANT:  Zagursky, Robert John
;  APPLICANT:  Metcalf, Benjamin J.
;  APPLICANT:  Peek, Joel A.
;  APPLICANT:  Sankaran, Banumathi
;  APPLICANT:  Fletcher, Leah Diane
;  TITLE OF INVENTION:  CHLAMYDIA TRACHOMATIS GENOMIC SEQUENCE
;  TITLE OF INVENTION:  AND POLYPEPTIDES, FRAGMENTS THEREOF AND USES THEREOF, IN
;  TITLE OF INVENTION:  PARTICULAR FOR THE DIAGNOSIS, PREVENTION AND TREATMENT OF
;  TITLE OF INVENTION:  INFECTION
;  FILE REFERENCE:  9710-0004-999
;  CURRENT APPLICATION NUMBER: US/09/201,228A
;  CURRENT FILING DATE:  1998-11-30
;  PRIOR APPLICATION NUMBER:  US 60/107,077
;  PRIOR FILING DATE:  1998-11-04
;  PRIOR APPLICATION NUMBER:  FR 97-16034
;  PRIOR FILING DATE:  1997-12-17
;  PRIOR APPLICATION NUMBER:  FR 97-15041
;  PRIOR FILING DATE:  1997-11-28
;  NUMBER OF SEQ ID NOS:  5981
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1038608
;   TYPE: DNA
;   ORGANISM: Chlamydia trachomatis
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1038608)
;   OTHER INFORMATION: n = A,T,C or G
US-09-201-228A-1

  Query Match             100.0%;  Score 20;  DB 16;  Length 1038608;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
              ||||||||||||||||||||
Db     635877 GGAGGAAGGCGAGGATGACG 635858


RESULT 6
US-10-289-762-1
; Sequence 1, Application US/10289762
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, prev
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
;   LENGTH: 1230025
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(15000)
;   OTHER INFORMATION: n=a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (15001)..(30000)
;   OTHER INFORMATION: n=a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (30001)..(45000)
;   OTHER INFORMATION: n=a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (45001)..(60000)
;   OTHER INFORMATION: n=a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (60001)..(75000)
;   OTHER INFORMATION: n=a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (75001)..(90000)
;   OTHER INFORMATION: n=a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (90001)..(105000)
;   OTHER INFORMATION: n=a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (105001)..(120000)
;   OTHER INFORMATION: n=a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (120001)..(135000)
;   OTHER INFORMATION: n=a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (135001)..(150000)
;   OTHER INFORMATION: n=a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (150001)..(165000)
;   OTHER INFORMATION: n=a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (165001)..(180000)
;   OTHER INFORMATION: n=a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (180001)..(195000)
;   OTHER INFORMATION: n=a or c or g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (195001)..(210000)
```

; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (210001)..(225000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (225001)..(240000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (240001)..(255000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (255001)..(270000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (270001)..(285000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (285001)..(300000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (300001)..(315000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (315001)..(330000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (330001)..(345000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (345001)..(360000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (360001)..(375000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (375001)..(390000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (390001)..(405000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (405001)..(420000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (420001)..(435000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (435001)..(450000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (450001)..(465000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (465001)..(480000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (480001)..(495000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (495001)..(510000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (510001)..(525000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (525001)..(540000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (540001)..(555000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (555001)..(570000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (570001)..(585000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (585001)..(600000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (600001)..(615000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (615001)..(630000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (630001)..(645000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (645001)..(660000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (660001)..(675000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (675001)..(690000)
; OTHER INFORMATION: n=a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature

Query Match 100.0%; Score 20; DB 48; Length 1230025;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAGGAAGGCGAGGATGACG 20
              ||||||||||||||||||||
Db    1011866 GGAGGAAGGCGAGGATGACG 1011885
```

RESULT 7
US-09-438-185-1
; Sequence 1, Application US/09438185
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard

```
;  APPLICANT:  Mitchell, Wayne
;  APPLICANT:  Kalman, Sue
;  APPLICANT:  Davis, Ronald
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION:  Chlamydia Pneumoniae Genome Sequence
;  FILE REFERENCE:  018941-000411US
;  CURRENT APPLICATION NUMBER: US/09/438,185
;  CURRENT FILING DATE:  1999-11-11
;  PRIOR APPLICATION NUMBER:  US 60/108,279
;  PRIOR FILING DATE:  1998-11-12
;  PRIOR APPLICATION NUMBER:  US 60/128,606
;  PRIOR FILING DATE:  1999-04-08
;  NUMBER OF SEQ ID NOS:  1074
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 1230230
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-09-438-185-1

  Query Match             100.0%;  Score 20;  DB 20;  Length 1230230;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
              ||||||||||||||||||||
Db    1001741 GGAGGAAGGCGAGGATGACG 1001760


RESULT 8
US-09-438-185A-1
; Sequence 1, Application US/09438185A
; GENERAL INFORMATION:
;  APPLICANT: Stephens, Richard
;  APPLICANT:  Mitchell, Wayne
;  APPLICANT:  Kalman, Sue
;  APPLICANT:  Davis, Ronald
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
;  FILE REFERENCE: 018941-000411US
;  CURRENT APPLICATION NUMBER: US/09/438,185A
;  CURRENT FILING DATE:  2002-03-13
;  PRIOR APPLICATION NUMBER: US 60/108,279
;  PRIOR FILING DATE: 1998-11-12
;  PRIOR APPLICATION NUMBER: US 60/128,606
;  PRIOR FILING DATE: 1999-04-08
;  NUMBER OF SEQ ID NOS: 1074
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 1230230
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-09-438-185A-1

  Query Match             100.0%;  Score 20;  DB 20;  Length 1230230;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
              ||||||||||||||||||||
Db    1001741 GGAGGAAGGCGAGGATGACG 1001760


RESULT 9
US-10-219-999-18302/c
; Sequence 18302, Application US/10219999
; GENERAL INFORMATION:
;  APPLICANT: Cao, Yongwei
;  APPLICANT:  Edgerton, Michael D
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Liu, Jingdong
;  APPLICANT:  Stein, Joshua
;  TITLE OF INVENTION: cDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
;  FILE REFERENCE: 38-10(52726)C
;  CURRENT APPLICATION NUMBER: US/10/219,999
;  CURRENT FILING DATE:  2002-08-15
;  PRIOR APPLICATION NUMBER: US 60/324,109
;  PRIOR FILING DATE: 2001-09-21
;  PRIOR APPLICATION NUMBER: US 60/312,544
;  PRIOR FILING DATE: 2001-08-15
;  NUMBER OF SEQ ID NOS: 63520
; SEQ ID NO 18302
;   LENGTH: 2123
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (161)..(1768)
;   OTHER INFORMATION:
US-10-219-999-18302

  Query Match             90.0%;  Score 18;  DB 47;  Length 2123;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGA 18
              ||||||||||||||||||
Db        305 GGAGGAAGGCGAGGATGA 288


RESULT 10
US-10-425-114-4575/c
; Sequence 4575, Application US/10425114
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 4575
;   LENGTH: 2123
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 700382382_FLI
US-10-425-114-4575

  Query Match             90.0%;  Score 18;  DB 51;  Length 2123;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGA 18
              ||||||||||||||||||
Db        305 GGAGGAAGGCGAGGATGA 288


RESULT 11
US-10-425-114A-4575/c
; Sequence 4575, Application US/10425114A
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
```

```
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114A
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 4575
;   LENGTH: 2123
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 700382382_FLI
US-10-425-114A-4575

  Query Match             90.0%;  Score 18;  DB 51;  Length 2123;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGA 18
              ||||||||||||||||||
Db        305 GGAGGAAGGCGAGGATGA 288


RESULT 12
US-10-437-963-25445/c
; Sequence 25445, Application US/10437963
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Wu, Wei
;  APPLICANT:  Boukharov, Andrey A.
;  APPLICANT:  Barbazuk, Brad
;  APPLICANT:  Li, Ping
;  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53221)B
;  CURRENT APPLICATION NUMBER: US/10/437,963
;  CURRENT FILING DATE:  2003-05-14
;  NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 25445
;   LENGTH: 2738
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_30330C.1
US-10-437-963-25445

  Query Match             90.0%;  Score 18;  DB 51;  Length 2738;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGA 18
              ||||||||||||||||||
Db        614 GGAGGAAGGCGAGGATGA 597


RESULT 13
US-09-702-134-21825/c
; Sequence 21825, Application US/09702134
; GENERAL INFORMATION:
;  APPLICANT:       Boukharov, Andrey A.
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Liu, Jingdong
;  APPLICANT:  McIninch, James
;  APPLICANT:  Wu, Wei
;  TITLE OF INVENTION:       Plant Genome Sequence and Uses Thereof
;  FILE REFERENCE:       38-21(51237)F
;  CURRENT APPLICATION NUMBER: US/09/702,134
;  CURRENT FILING DATE:  2000-10-31
;  NUMBER OF SEQ ID NOS:       52202
; SEQ ID NO 21825
;   LENGTH: 13218
;   TYPE: DNA
;   ORGANISM: Oryza sativa
US-09-702-134-21825

  Query Match             90.0%;  Score 18;  DB 30;  Length 13218;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGA 18
              ||||||||||||||||||
Db        103 GGAGGAAGGCGAGGATGA 86


RESULT 14
US-09-815-264-71774/c
; Sequence 71774, Application US/09815264
; GENERAL INFORMATION:
;  APPLICANT: Boukharov, Andrey A.
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Dotson, Stanton B.
;  APPLICANT:  Koshi, Jeffrey M.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Liu, Jingdong
;  APPLICANT:  McIninch, James
;  APPLICANT:  Wu, Wei
;  TITLE OF INVENTION: Genomic Plant Sequences And Uses Thereof
;  FILE REFERENCE: 38-21(51237)G
;  CURRENT APPLICATION NUMBER: US/09/815,264
;  CURRENT FILING DATE:  2001-03-23
;  PRIOR APPLICATION NUMBER: US 09/620,392
;  PRIOR FILING DATE: 2000-07-19
;  PRIOR APPLICATION NUMBER: US 09/702,134
;  PRIOR FILING DATE: 2000-10-31
;  NUMBER OF SEQ ID NOS: 109669
; SEQ ID NO 71774
;   LENGTH: 13218
;   TYPE: DNA
;   ORGANISM: Oryza sativa
US-09-815-264-71774

  Query Match             90.0%;  Score 18;  DB 33;  Length 13218;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGA 18
              ||||||||||||||||||
Db        103 GGAGGAAGGCGAGGATGA 86


RESULT 15
US-09-620-392-33867/c
; Sequence 33867, Application US/09620392
; GENERAL INFORMATION:
;  APPLICANT:       Boukharov, Andrey A.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Liu, Jingdong
;  APPLICANT:  McIninch, James
;  TITLE OF INVENTION:       Plant Genome Sequence And Uses Thereof
;  FILE REFERENCE:       38-21(51237)E
;  CURRENT APPLICATION NUMBER: US/09/620,392
;  CURRENT FILING DATE:  2000-07-19
;  NUMBER OF SEQ ID NOS:       69652
; SEQ ID NO 33867
;   LENGTH: 13263
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;   OTHER INFORMATION: unsure at all n locations
US-09-620-392-33867

  Query Match             90.0%;  Score 18;  DB 26;  Length 13263;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 GGAGGAAGGCGAGGATGA 18
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Db        103 GGAGGAAGGCGAGGATGA 86
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Search completed: August 4, 2004, 11:29:54
Job time : 1831.78 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 04:03:11 ; Search time 963.229 Seconds
(without alignments)
989.948 Million cell updates/sec

Title: US-09-940-860-3
Perfect score: 22
Sequence: 1 acaaggcccgagaacgtattca 22

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	22	100.0	236	1	AF294958	AF294958 Uncultur
c	2	22	100.0	260	1	AF389905	AF389905 Uncultur
c	3	22	100.0	302	1	AY391637	AY391637 Uncultur
c	4	22	100.0	302	1	AY391643	AY391643 Uncultur
c	5	22	100.0	309	1	AY391670	AY391670 Uncultur
c	6	22	100.0	368	6	AR071569	AR071569 Sequence
c	7	22	100.0	370	6	AR071568	AR071568 Sequence
c	8	22	100.0	372	1	AF257294	AF257294 Uncultur
c	9	22	100.0	380	13	UMI241780	AJ241780 Unidentif
	10	22	100.0	420	3	AF535201	AF535201 Uncultur
	11	22	100.0	431	1	AF226208	AF226208 Uncultur
c	12	22	100.0	432	1	AY191889	AY191889 Uncultur
c	13	22	100.0	458	1	AB041277	AB041277 Uncultur
c	14	22	100.0	473	1	AF385928	AF385928 Mobiluncu
c	15	22	100.0	497	1	AF289914	AF289914 Uncultur
c	16	22	100.0	498	6	AR071534	AR071534 Sequence
c	17	22	100.0	499	1	AXXRG16SC	L09057 Unknown ana
	18	22	100.0	500	3	AY038517	AY038517 Uncultur
c	19	22	100.0	510	1	AB075168	AB075168 Uncultur
c	20	22	100.0	519	1	AY261423	AY261423 Uncultur
c	21	22	100.0	527	1	AY090655	AY090655 Uncultur
c	22	22	100.0	550	1	AF449786	AF449786 Uncultur
c	23	22	100.0	562	1	AF027037	AF027037 Unidentif
c	24	22	100.0	584	13	UMI241721	AJ241721 Unidentif
c	25	22	100.0	600	1	AF332350	AF332350 Uncultur
c	26	22	100.0	600	1	AF429144	AF429144 Uncultur
c	27	22	100.0	600	1	AF429158	AF429158 Uncultur
c	28	22	100.0	600	1	AF429234	AF429234 Uncultur
c	29	22	100.0	604	1	AY012520S2	AY012521 Uncultur
c	30	22	100.0	626	1	AF027077	AF027077 Unidentif
	31	22	100.0	633	1	AY235614	AY235614 Uncultur
c	32	22	100.0	645	1	AF320943S2	AF320944 Uncultur
	33	22	100.0	655	1	AY217417	AY217417 Uncultur
c	34	22	100.0	673	1	AF320967S2	AF320968 Uncultur
	35	22	100.0	681	1	AY235670	AY235670 Uncultur
c	36	22	100.0	689	1	AY100537	AY100537 Uncultur
c	37	22	100.0	695	1	AF422641	AF422641 Uncultur
c	38	22	100.0	695	1	AF424241	AF424241 Uncultur
c	39	22	100.0	699	1	AF422682	AF422682 Uncultur
c	40	22	100.0	719	1	UBZ94006	Z94006 Unidentifie
c	41	22	100.0	739	1	AY133110	AY133110 Uncultur
c	42	22	100.0	760	1	AF424258	AF424258 Uncultur
c	43	22	100.0	760	1	AY239544	AY239544 Uncultur
c	44	22	100.0	762	1	AF422623	AF422623 Uncultur
c	45	22	100.0	781	1	AY239537	AY239537 Uncultur

ALIGNMENTS

RESULT 1
AF294958/c
LOCUS AF294958 236 bp DNA linear BCT 10-JAN-2002
DEFINITION Uncultured eubacterium OTU1 16S ribosomal RNA gene, partial sequence.
ACCESSION AF294958
VERSION AF294958.1 GI:15419629
KEYWORDS .
SOURCE uncultured eubacterium
ORGANISM uncultured eubacterium
Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 236)
AUTHORS Cutter,L.A., Watts,J.E., Sowers,K.R. and May,H.D.
TITLE Identification of a microorganism that links its growth to the reductive dechlorination of 2,3,5,6-chlorobiphenyl

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  JOURNAL   Environ. Microbiol. 3 (11), 699-709 (2001)
  MEDLINE   21835716
   PUBMED   11846760
REFERENCE   2  (bases 1 to 236)
  AUTHORS   Cutter,L.A., Watts,J.E.M., Sowers,K.R. and May,H.D.
  TITLE     Indications for acetate as the carbon source and electron donor in
            anaerobic ortho PCB dechlorination
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 236)
  AUTHORS   Watts,J.E.M., Cutter,L.A., Sowers,K.R. and May,H.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-AUG-2000) Center of Marine Biotechnology, 701 E.
            Pratt St., Baltimore, MD 21202, USA
FEATURES             Location/Qualifiers
     source          1. .236
                     /organism="uncultured eubacterium"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:73429"
                     /note="OTU 1; PCB dechlorinating culture"
     rRNA            <1. .>236
                     /product="16S ribosomal RNA"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 4.4;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        207 ACAAGGCCCGAGAACGTATTCA 186


RESULT 2
AF389905/c
LOCUS       AF389905                 260 bp    DNA     linear   BCT 10-FEB-2002
DEFINITION  Uncultured green sulfur bacterium clone OTU 1 16S ribosomal RNA
            gene, partial sequence.
ACCESSION   AF389905
VERSION     AF389905.1  GI:18643063
KEYWORDS    .
SOURCE      uncultured Chlorobi bacterium
  ORGANISM  uncultured Chlorobi bacterium
            Bacteria; Chlorobi; environmental samples.
REFERENCE   1  (bases 1 to 260)
  AUTHORS   Wu,Q., Watts,J.E., Sowers,K.R. and May,H.D.
  TITLE     Identification of a bacterium that specifically catalyzes the
            reductive dechlorination of polychlorinated biphenyls with doubly
            flanked chlorines
  JOURNAL   Appl. Environ. Microbiol. 68 (2), 807-812 (2002)
  MEDLINE   21681065
   PUBMED   11823222
REFERENCE   2  (bases 1 to 260)
  AUTHORS   Watts,J.E.M., Wu,Q., May,H.D. and Sowers,K.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUN-2001) Center of Marine Biotechnology, University
            of Maryland Biotechnology Institute, Columbus Center, 701 E. Pratt
            St., Baltimore, MD 21202, USA
FEATURES             Location/Qualifiers
     source          1. .260
                     /organism="uncultured Chlorobi bacterium"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:156405"
                     /clone="OTU 1"
                     /note="DNA sequence from PCB-dechlorinating enrichment
                     culture"
     rRNA            <1. .>260
                     /product="16S ribosomal RNA"
ORIGIN

  Query Match           100.0%;  Score 22;  DB 1;  Length 260;
  Best Local Similarity   100.0%;  Pred. No. 4.3;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        207 ACAAGGCCCGAGAACGTATTCA 186


RESULT 3
AY391637/c
LOCUS       AY391637                 302 bp    DNA     linear   BCT 15-OCT-2003
DEFINITION  Uncultured soil bacterium clone M21 16S ribosomal RNA gene, partial
            sequence.
ACCESSION   AY391637
VERSION     AY391637.1  GI:37624038
KEYWORDS    .
SOURCE      uncultured soil bacterium
  ORGANISM  uncultured soil bacterium
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 302)
  AUTHORS   Sun,H., Deng,S. and Raun,W.R.
  TITLE     Microbiology community structure and diversity in a century-long
            manure-treated agroecosystem
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 302)
  AUTHORS   Sun,H., Deng,S. and Raun,W.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-SEP-2003) Plant and Soil Sciences, Oklahoma State
            University, 368 Ag Hall, Stillwater, OK 74078, USA
FEATURES             Location/Qualifiers
     source          1. .302
                     /organism="uncultured soil bacterium"
                     /mol_type="genomic DNA"
                     /isolation_source="total microbial community of
                     century-long manure-treated soil"
                     /db_xref="taxon:164851"
                     /clone="M21"
                     /environmental_sample
     rRNA            <1. .>302
                     /product="16S ribosomal RNA"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        289 ACAAGGCCCGAGAACGTATTCA 268


RESULT 4
AY391643/c
LOCUS       AY391643                 302 bp    DNA     linear   BCT 15-OCT-2003
DEFINITION  Uncultured soil bacterium clone M27 16S ribosomal RNA gene, partial
            sequence.
ACCESSION   AY391643
VERSION     AY391643.1  GI:37624044
KEYWORDS    .
SOURCE      uncultured soil bacterium
  ORGANISM  uncultured soil bacterium
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 302)
  AUTHORS   Sun,H., Deng,S. and Raun,W.R.
  TITLE     Microbiology community structure and diversity in a century-long
            manure-treated agroecosystem
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 302)
  AUTHORS   Sun,H., Deng,S. and Raun,W.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-SEP-2003) Plant and Soil Sciences, Oklahoma State
            University, 368 Ag Hall, Stillwater, OK 74078, USA
FEATURES             Location/Qualifiers
     source          1. .302
                     /organism="uncultured soil bacterium"
                     /mol_type="genomic DNA"
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                     /isolation_source="total microbial community of
                     century-long manure-treated soil"
                     /db_xref="taxon:164851"
                     /clone="M27"
                     /environmental_sample
     rRNA            <1. .>302
                     /product="16S ribosomal RNA"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 1;  Length 302;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        289 ACAAGGCCCGAGAACGTATTCA 268


RESULT 5
AY391670/c
LOCUS       AY391670                309 bp    DNA     linear   BCT 15-OCT-2003
DEFINITION  Uncultured soil bacterium clone M54 16S ribosomal RNA gene, partial
            sequence.
ACCESSION   AY391670
VERSION     AY391670.1  GI:37624071
KEYWORDS    .
SOURCE      uncultured soil bacterium
  ORGANISM  uncultured soil bacterium
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 309)
  AUTHORS   Sun,H., Deng,S. and Raun,W.R.
  TITLE     Microbiology community structure and diversity in a century-long
            manure-treated agroecosystem
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 309)
  AUTHORS   Sun,H., Deng,S. and Raun,W.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-SEP-2003) Plant and Soil Sciences, Oklahoma State
            University, 368 Ag Hall, Stillwater, OK 74078, USA
FEATURES             Location/Qualifiers
     source          1. .309
                     /organism="uncultured soil bacterium"
                     /mol_type="genomic DNA"
                     /isolation_source="total microbial community of
                     century-long manure-treated soil"
                     /db_xref="taxon:164851"
                     /clone="M54"
                     /environmental_sample
     rRNA            <1. .>309
                     /product="16S ribosomal RNA"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 1;  Length 309;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        296 ACAAGGCCCGAGAACGTATTCA 275


RESULT 6
AR071569/c
LOCUS       AR071569                368 bp    DNA     linear   PAT 18-FEB-2000
DEFINITION  Sequence 36 from patent US 5912117.
ACCESSION   AR071569
VERSION     AR071569.1  GI:7222457
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 368)
  AUTHORS   Dodge,D.E. and White,T.J.
  TITLE     Method for diagnosis of lyme disease
  JOURNAL   Patent: US 5912117-A 36 15-JUN-1999;
FEATURES             Location/Qualifiers
     source          1. .368
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        273 ACAAGGCCCGAGAACGTATTCA 252


RESULT 7
AR071568/c
LOCUS       AR071568                370 bp    DNA     linear   PAT 18-FEB-2000
DEFINITION  Sequence 35 from patent US 5912117.
ACCESSION   AR071568
VERSION     AR071568.1  GI:7222456
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 370)
  AUTHORS   Dodge,D.E. and White,T.J.
  TITLE     Method for diagnosis of lyme disease
  JOURNAL   Patent: US 5912117-A 35 15-JUN-1999;
FEATURES             Location/Qualifiers
     source          1. .370
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 370;
  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        275 ACAAGGCCCGAGAACGTATTCA 254


RESULT 8
AF257294/c
LOCUS       AF257294                372 bp    DNA     linear   BCT 09-JUL-2001
DEFINITION  Uncultured marine gamma proteobacterium DHB-31 16S ribosomal RNA
            gene, partial sequence.
ACCESSION   AF257294
VERSION     AF257294.1  GI:14317937
KEYWORDS    .
SOURCE      uncultured marine gamma proteobacterium DHB-31
  ORGANISM  uncultured marine gamma proteobacterium DHB-31
            Bacteria; Proteobacteria; Gammaproteobacteria; environmental
            samples.
REFERENCE   1  (bases 1 to 372)
  AUTHORS   Lopez-Garcia,P., Lopez-Lopez,A., Moreira,D. and Rodriguez-Valera,F.
  TITLE     Diversity of free-living prokaryotes from a deep-sea site at the
            Antarctic Polar Front
  JOURNAL   FEMS Microbiol. Ecol. 36 (2-3), 193-202 (2001)
   PUBMED   11451524
REFERENCE   2  (bases 1 to 372)
  AUTHORS   Lopez-Garcia,P., Lopez-Lopez,A., Moreira,D. and Rodriguez-Valera,F.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-APR-2000) Microbiology, University Miguel Hernandez,
            Facultad de Medicina, Campus de San Juan, San Juan, Alicante 03550,
            Spain
FEATURES             Location/Qualifiers
     source          1. .372
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:123962"
                     /clone="DHB-31"
     rRNA            <1. .>372
                     /product="16S ribosomal RNA"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        259 ACAAGGCCCGAGAACGTATTCA 238


RESULT 9
UMI241780/c
LOCUS       UMI241780               380 bp    DNA     linear   UNA 12-DEC-1999
DEFINITION  Unidentified microorganism 16S rRNA gene, partial, clone Cow39.
ACCESSION   AJ241780
VERSION     AJ241780.1  GI:6066808
KEYWORDS    16S ribosomal RNA; 16S rRNA gene.
SOURCE      unidentified microorganism
  ORGANISM  unidentified microorganism
            unclassified; environmental samples.
REFERENCE   1  (bases 1 to 380)
  AUTHORS   Pryde,S.E., Richardson,A.J., Stewart,C.S. and Flint,H.J.
  TITLE     Molecular analysis of the microbial diversity present in the
            colonic wall, colonic lumen, and cecal lumen of a pig
  JOURNAL   Appl. Environ. Microbiol. 65 (12), 5372-5377 (1999)
  MEDLINE   20049972
   PUBMED   10583991
REFERENCE   2  (bases 1 to 380)
  AUTHORS   Pryde,S.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-APR-1999) Pryde S.E., Microbial and Intestinal
            biology, Rowett Research Institute, Greenburn Road, Bucksburn,
            Aberdeen, AB21 9SB, UK
FEATURES             Location/Qualifiers
     source          1. .380
                     /organism="unidentified microorganism"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:81726"
                     /clone="Cow39"
     gene            1. .380
                     /gene="16S rRNA"
     rRNA            <1. .>380
                     /gene="16S rRNA"
                     /product="16S ribosomal RNA"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 13;  Length 380;
  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        288 ACAAGGCCCGAGAACGTATTCA 267


RESULT 10
AF535201
LOCUS       AF535201                420 bp    DNA     linear   INV 09-SEP-2002
DEFINITION  Uncultured euglenid clone CD1H11 16S ribosomal RNA gene, partial
            sequence.
ACCESSION   AF535201
VERSION     AF535201.1  GI:22758963
KEYWORDS    .
SOURCE      uncultured euglenid
  ORGANISM  uncultured euglenid
            Eukaryota; Euglenozoa; environmental samples.
REFERENCE   1  (bases 1 to 420)
  AUTHORS   Frias-Lopez,J., Zerkle,A.L., Bonheyo,G.T. and Fouke,B.W.
  TITLE     Partitioning of bacterial communities between seawater and healthy,
            black band diseased, and dead coral surfaces
  JOURNAL   Appl. Environ. Microbiol. 68 (5), 2214-2228 (2002)
  MEDLINE   21972269
   PUBMED   11976091
REFERENCE   2  (bases 1 to 420)
  AUTHORS   Frias-Lopez,J., Zerkle,A.L., Bonheyo,G.T. and Fouke,B.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-AUG-2002) Department of Geology, University of
            Illinois at Urbana-Champaign, 1301 W. Green Street, Urbana, IL
            61801, USA
FEATURES             Location/Qualifiers
     source          1. .420
                     /organism="uncultured euglenid"
                     /mol_type="genomic DNA"
                     /isolation_source="marine"
                     /db_xref="taxon:167168"
                     /clone="CD1H11"
                     /environmental_sample
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                     /product="16S ribosomal RNA"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 3;  Length 420;
  Best Local Similarity   100.0%;  Pred. No. 3.7;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db         38 ACAAGGCCCGAGAACGTATTCA 59


RESULT 11
AF226208
LOCUS       AF226208                431 bp    DNA     linear   BCT 28-MAY-2002
DEFINITION  Uncultured maize root bacterium Zmrc163 16S ribosomal RNA gene,
            partial sequence.
ACCESSION   AF226208
VERSION     AF226208.1  GI:7716143
KEYWORDS    .
SOURCE      uncultured maize root bacterium Zmrc163
  ORGANISM  uncultured maize root bacterium Zmrc163
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 431)
  AUTHORS   Chelius,M.K. and Triplett,E.W.
  TITLE     The Diversity of Archaea and Bacteria in Association with the Roots
            of Zea mays L
  JOURNAL   Microb. Ecol. 41 (3), 252-263 (2001)
   PUBMED   11391463
REFERENCE   2  (bases 1 to 431)
  AUTHORS   Chelius,M.K. and Triplett,E.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-JAN-2000) Agronomy, University of Wisconsin-Madison,
            1575 Linden Dr., Madison, WI 53706, USA
FEATURES             Location/Qualifiers
     source          1. .431
                     /organism="uncultured maize root bacterium Zmrc163"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:121653"
                     /clone="Zmrc163"
     rRNA            complement(<1. .>431)
                     /product="16S ribosomal RNA"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 1;  Length 431;
  Best Local Similarity   100.0%;  Pred. No. 3.7;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db         73 ACAAGGCCCGAGAACGTATTCA 94
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RESULT 12
AY191889/c
LOCUS       AY191889                 432 bp    DNA     linear   BCT 10-MAR-2003
DEFINITION  Uncultured bacterium clone BG6 16S ribosomal RNA gene, partial
            sequence.
ACCESSION   AY191889
VERSION     AY191889.1  GI:28396218
KEYWORDS    .
SOURCE      uncultured bacterium
  ORGANISM  uncultured bacterium
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 432)
  AUTHORS   Macur,R.E., Langner,H.W. and Inskeep,W.P.
  TITLE     Molecular analysis of microbial communities in
            acid-sulfate-chloride-arsenic geothermal springs in Yellowstone
            National Park
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 432)
  AUTHORS   Macur,R.E., Langner,H.W. and Inskeep,W.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-DEC-2002) Land Resources and Environmental Sciences,
            Montana State University - Bozeman, Leon Johnson Hall, Bozeman, MT
            59717, USA
FEATURES             Location/Qualifiers
     source          1. .432
                     /organism="uncultured bacterium"
                     /mol_type="genomic DNA"
                     /isolation_source="acid-sulfate-chloride-arsenic
                     geothermal spring"
                     /db_xref="taxon:77133"
                     /clone="BG6"
                     /environmental_sample
                     /country="USA: Wyoming, Yellowstone National Park"
     rRNA            <1. .>432
                     /product="16S ribosomal RNA"
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 3.7;
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Qy          1 ACAAGGCCCGAGAACGTATTCA 22
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Db        419 ACAAGGCCCGAGAACGTATTCA 398


RESULT 13
AB041277/c
LOCUS       AB041277                 458 bp    DNA     linear   BCT 29-NOV-2002
DEFINITION  Uncultured bacterium ECS7 gene for 16S ribosomal RNA, partial
            sequence.
ACCESSION   AB041277
VERSION     AB041277.1  GI:10716064
KEYWORDS    .
SOURCE      uncultured bacterium ECS7
  ORGANISM  uncultured bacterium ECS7
            Bacteria; environmental samples.
REFERENCE   1
  AUTHORS   Sekiguchi,H., Koshikawa,H., Hiroki,M., Murakami,S., Xu,K.,
            Watanabe,M., Nakahara,T., Zhu,M. and Uchiyama,H.
  TITLE     Bacterial distribution and phylogenetic diversity in the Changjiang
            estuary before the construction of the Three Gorges Dam
  JOURNAL   Microb. Ecol. 43 (1), 82-91 (2002)
  MEDLINE   22088774
   PUBMED   11984631
REFERENCE   2  (bases 1 to 458)
  AUTHORS   Sekiguchi,H. and Uchiyama,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-APR-2000) Hiroyuki Sekiguchi, National Institute for
            Environmental Studies, Water Environmet Quality; Onogawa16-2,
            Tsukuba, Ibaraki 305-0053, Japan (E-mail:seki@nies.go.jp,
            Tel:81-298-50-2412, Fax:81-298-50-2576)
FEATURES             Location/Qualifiers
     source          1. .458
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                     /mol_type="genomic DNA"
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     rRNA            <1. .>458
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ORIGIN

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Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        360 ACAAGGCCCGAGAACGTATTCA 339


RESULT 14
AF385928/c
LOCUS       AF385928                 473 bp    DNA     linear   BCT 02-JAN-2003
DEFINITION  Mobiluncus mulieris 16S-23S ribosomal RNA intergenic spacer,
            partial sequence.
ACCESSION   AF385928
VERSION     AF385928.1  GI:27462290
KEYWORDS    .
SOURCE      Mobiluncus mulieris
  ORGANISM  Mobiluncus mulieris
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Actinomycineae; Actinomycetaceae; Mobiluncus.
REFERENCE   1  (bases 1 to 473)
  AUTHORS   Park,H., Kim,C., Choi,H., Jang,H. and Kim,H.
  TITLE     Mobiluncus curtisii DNA for 16S-23S rRNA internal transcribed
            spacer
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 473)
  AUTHORS   Park,H., Kim,C., Choi,H., Jang,H. and Kim,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-MAY-2001) SJ Hightech Co., Ltd., College of Medicine,
            Pusan National University, 10 Amidong-1-Ga, Seogu, Pusan 602-739,
            Korea
FEATURES             Location/Qualifiers
     source          1. .473
                     /organism="Mobiluncus mulieris"
                     /mol_type="genomic DNA"
                     /strain="ATCC35243"
                     /db_xref="ATCC:35243"
                     /db_xref="taxon:2052"
     misc_RNA        <1. .>473
                     /product="16S-23S ribosomal RNA intergenic spacer"
ORIGIN

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Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db         33 ACAAGGCCCGAGAACGTATTCA 12


RESULT 15
AF289914/c
LOCUS       AF289914                 497 bp    DNA     linear   BCT 09-APR-2001
DEFINITION  Uncultured green nonsulfur bacterium Kmlps6-20 16S ribosomal RNA
            gene, partial sequence.
ACCESSION   AF289914
VERSION     AF289914.1  GI:9937457
KEYWORDS    .
SOURCE      uncultured green non-sulfur bacterium Kmlps6-20
  ORGANISM  uncultured green non-sulfur bacterium Kmlps6-20
            Bacteria; Chloroflexi; environmental samples.
```

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REFERENCE   1  (bases 1 to 488)
  AUTHORS   Yu,Z. and Mohn,W.W.
  TITLE     Bacterial diversity and community structure in an aerated lagoon
            revealed by ribosomal intergenic spacer analyses and 16S ribosomal
            DNA sequencing
  JOURNAL   Appl. Environ. Microbiol. 67 (4), 1565-1574 (2001)
  MEDLINE   21178505
   PUBMED   11282606
REFERENCE   2  (bases 1 to 497)
  AUTHORS   Yu,Z. and Mohn,W.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-JUL-2000) Microbiology and Immunology, University of
            British Columbia, #300-6174 University Blvd., Vancouver, BC V6T
            1Z3, Canada
FEATURES             Location/Qualifiers
     source          1. .497
                     /organism="uncultured green non-sulfur bacterium
                     Kmlps6-20"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:135383"
                     /clone="Kmlps6-20"
     rRNA            <1. .>497
                     /product="16S ribosomal RNA"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 3.6;
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Qy          1 ACAAGGCCCGAGAACGTATTCA 22
              ||||||||||||||||||||||
Db        472 ACAAGGCCCGAGAACGTATTCA 451


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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 04:03:11 ; Search time 875.663 Seconds
(without alignments)
989.948 Million cell updates/sec

Title: US-09-940-860-2
Perfect score: 20
Sequence: 1 ggaggaaggcgaggatgacg 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
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35: em_htg_rod:*
36: em_htg_mam:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	570	1	AB018671	AB018671 Endosymbi
2	20	100.0	601	1	AF507717	AF507717 Unculture
3	20	100.0	617	1	AY369151	AY369151 Unculture
4	20	100.0	827	1	AF317470	AF317470 Candidatu
5	20	100.0	857	1	AY220719	AY220719 Unculture
6	20	100.0	902	1	UBA309645	AJ309645 Unculture
7	20	100.0	910	1	UBA309647	AJ309647 Unculture
8	20	100.0	911	1	UBA309611	AJ309611 Unculture
9	20	100.0	936	1	AF050608	AF050608 Unculture
10	20	100.0	1247	1	UBA519648	AJ519648 Unculture
11	20	100.0	1255	1	AF524023	AF524023 Unculture
12	20	100.0	1298	1	APBRGDC	L35460 Alpha prote
13	20	100.0	1313	1	AB088955	AB088955 Unculture
14	20	100.0	1318	1	AF229791	AF229791 Unculture
15	20	100.0	1335	1	AF127027	AF127027 Helicobac
16	20	100.0	1354	1	CPU73782	U73782 Chlamydia p
17	20	100.0	1354	1	CPU73785	U73785 Chlamydia p
18	20	100.0	1355	1	CPU73783	U73783 Chlamydia p
19	20	100.0	1383	1	AY126640	AY126640 Endosymbi
20	20	100.0	1433	1	AY328728	AY328728 Unculture
21	20	100.0	1445	1	AF382129	AF382129 Unculture
22	20	100.0	1446	1	MBA400342	AJ400342 Unculture
23	20	100.0	1447	1	AF382141	AF382141 Unculture
24	20	100.0	1457	1	CPIOL16SR	Z49874 C.pneumonia
25	20	100.0	1466	1	CPEAE16SR	Z49871 Chlamydophi
26	20	100.0	1466	1	CPOAE16SR	Z49872 Chlamydophi
27	20	100.0	1468	1	AF507685	AF507685 Unculture
28	20	100.0	1471	1	UAU75649	U75649 Unidentifie
29	20	100.0	1479	1	CPTW183RR	Z49873 C.pneumonia
30	20	100.0	1480	1	UEU408994	AJ408994 Unculture
31	20	100.0	1492	1	AY328720	AY328720 Unculture
32	20	100.0	1507	1	AB001778	AB001778 Chlamydop
33	20	100.0	1507	1	AB001779	AB001779 Chlamydop
34	20	100.0	1507	1	AB001780	AB001780 Chlamydop
35	20	100.0	1507	1	AB001781	AB001781 Chlamydop
36	20	100.0	1507	1	AB001782	AB001782 Chlamydop
37	20	100.0	1507	1	AB001783	AB001783 Chlamydop
38	20	100.0	1507	1	AB001784	AB001784 Chlamydop
39	20	100.0	1507	1	AB001785	AB001785 Chlamydop
40	20	100.0	1507	1	AB001786	AB001786 Chlamydop
41	20	100.0	1507	1	AB001787	AB001787 Chlamydop
42	20	100.0	1507	1	AB001788	AB001788 Chlamydop
43	20	100.0	1507	1	AB001789	AB001789 Chlamydop
44	20	100.0	1507	1	AB001790	AB001790 Chlamydop
45	20	100.0	1507	1	AB001791	AB001791 Chlamydop

ALIGNMENTS

RESULT 1
AB018671
LOCUS AB018671 570 bp DNA linear BCT 03-APR-1999
DEFINITION Endosymbiont of Camponotus kiusiuensis gene for 16S ribosomal RNA, partial sequence.
ACCESSION AB018671
VERSION AB018671.1 GI:4587318
KEYWORDS 16S rRNA.
SOURCE endosymbiont of Camponotus kiusiuensis
ORGANISM endosymbiont of Camponotus kiusiuensis
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.
REFERENCE 1 (sites)
AUTHORS Sameshima,S., Hasegawa,E., Kitade,O., Minaka,N. and Matsumoto,T.
TITLE Phylogenetic comparison of the endosymbionts with their host ants

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            based on molecular evidences
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 570)
  AUTHORS   Sameshima,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-OCT-1998) Shinya Sameshima, University of Tokyo,
            Department of Biology; 3-8-1 Komaba, Meguro-ku, Tokyo 153-8902,
            Japan (E-mail:ss77216@hongo.ecc.u-tokyo.ac.jp, Tel:+81-3-5454-6652,
            Fax:+81-3-5454-4322)
FEATURES             Location/Qualifiers
     source          1. .570
                     /organism="endosymbiont of Camponotus kiusiuensis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:84570"
     rRNA            <1. .>570
                     /product="16S ribosomal RNA"
ORIGIN

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Qy          1 GGAGGAAGGCGAGGATGACG 20
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Db        355 GGAGGAAGGCGAGGATGACG 374


RESULT 2
AF507717
LOCUS       AF507717                601 bp    DNA     linear   BCT 03-JUN-2002
DEFINITION  Uncultured soil bacterium clone S13 16S ribosomal RNA gene, partial
            sequence.
ACCESSION   AF507717
VERSION     AF507717.1  GI:20978172
KEYWORDS    .
SOURCE      uncultured soil bacterium
  ORGANISM  uncultured soil bacterium
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 601)
  AUTHORS   Dunbar,J., Barns,S.M., Ticknor,L.O. and Kuske,C.R.
  TITLE     Empirical and theoretical bacterial diversity in four Arizona soils
  JOURNAL   Appl. Environ. Microbiol. 68 (6), 3035-3045 (2002)
  MEDLINE   22034980
   PUBMED   12039765
REFERENCE   2  (bases 1 to 601)
  AUTHORS   Dunbar,J., Barns,S.M., Ticknor,L.O. and Kuske,C.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-APR-2002) Biosciences Division, Los Alamos National
            Laboratory, M888, Los Alamos, NM 87545, USA
FEATURES             Location/Qualifiers
     source          1. .601
                     /organism="uncultured soil bacterium"
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                     /isolation_source="pinyon-juniper forest soil"
                     /db_xref="taxon:164851"
                     /clone="S13"
                     /environmental_sample
     rRNA            <1. .>601
                     /product="16S ribosomal RNA"
ORIGIN

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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
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Db        385 GGAGGAAGGCGAGGATGACG 404


RESULT 3
AY369151
LOCUS       AY369151                617 bp    DNA     linear   BCT 14-SEP-2003
DEFINITION  Uncultured bacterium clone F-OTU12 16S ribosomal RNA gene, partial
            sequence.
ACCESSION   AY369151
VERSION     AY369151.1  GI:34555665
KEYWORDS    .
SOURCE      uncultured bacterium
  ORGANISM  uncultured bacterium
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 617)
  AUTHORS   Zheng,X., Yang,H. and Li,D.
  TITLE     Analysis of the microbial community composition and transition in
            the activated sludge of a lab-scale deammonification reactor by
            molecular methods
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 617)
  AUTHORS   Zheng,X., Yang,H. and Li,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-AUG-2003) School of Life Science and Technology,
            Shanghai Jiaotong University, No.800, Dongchuan Road, Shanghai
            200240, China
FEATURES             Location/Qualifiers
     source          1. .617
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:77133"
                     /clone="F-OTU12"
                     /environmental_sample
     rRNA            <1. .>617
                     /product="16S ribosomal RNA"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 1;  Length 617;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
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Db        252 GGAGGAAGGCGAGGATGACG 271


RESULT 4
AF317470
LOCUS       AF317470                827 bp    DNA     linear   BCT 04-FEB-2002
DEFINITION  Candidatus Helicobacter bovis strain Toro3A 16S ribosomal RNA gene,
            partial sequence.
ACCESSION   AF317470
VERSION     AF317470.1  GI:18482505
KEYWORDS    .
SOURCE      Candidatus Helicobacter bovis
  ORGANISM  Candidatus Helicobacter bovis
            Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
            Helicobacteraceae; Helicobacter.
REFERENCE   1  (bases 1 to 827)
  AUTHORS   Gueneau,P., Fuenmayor,J., Aristimuno,O.C., Cedeno,S., Baez,E.,
            Reyes,N., Michelangeli,F. and Dominguez-Bello,M.G.
  TITLE     Are goats naturally resistant to gastric Helicobacter infection?
  JOURNAL   Vet. Microbiol. 84 (1-2), 115-121 (2002)
  MEDLINE   21589087
   PUBMED   11731164
REFERENCE   2  (bases 1 to 827)
  AUTHORS   Gueneau de Novoa,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-OCT-2000) CBB, IVIC, Km 11 Panamericana, Altos de
            Pipe Miranda, Venezuela
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /strain="Toro3A"
                     /db_xref="taxon:104629"
                     /note="sequence derived from a single PCR amplicon
                     obtained from the gastric mucosa of a bull from Venezuela"
     rRNA            <1. .>827
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                     /product="16S ribosomal RNA"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 37;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
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Db        713 GGAGGAAGGCGAGGATGACG 732


RESULT 5
AY220719
LOCUS       AY220719                 857 bp    DNA     linear   BCT 09-FEB-2003
DEFINITION  Uncultured alpha proteobacterium clone WCPAP15 16S ribosomal RNA
            gene, partial sequence.
ACCESSION   AY220719
VERSION     AY220719.1  GI:28274894
KEYWORDS    .
SOURCE      uncultured alpha proteobacterium
  ORGANISM  uncultured alpha proteobacterium
            Bacteria; Proteobacteria; Alphaproteobacteria; environmental
            samples.
REFERENCE   1  (bases 1 to 857)
  AUTHORS   Gallagher,J.M., Carton,M., Eardly,D.F. and Patching,J.W.
  TITLE     Prokaryotic community structure and biodiversity in deep waters of
            the NE Atlantic
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 857)
  AUTHORS   Gallagher,J.M., Carton,M., Eardly,D.F. and Patching,J.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JAN-2003) Microbiology, NUI, Galway, University Rd.,
            Galway, Rep. of Ireland
FEATURES             Location/Qualifiers
     source          1. .857
                     /organism="uncultured alpha proteobacterium"
                     /mol_type="genomic DNA"
                     /isolation_source="water column, Porcupine Abyssal Plain,
                     Northeast Atlantic Ocean"
                     /db_xref="taxon:91750"
                     /clone="WCPAP15"
                     /environmental_sample
     rRNA            <1. .>857
                     /product="16S ribosomal RNA"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 1;  Length 857;
  Best Local Similarity   100.0%;  Pred. No. 36;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
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Db        641 GGAGGAAGGCGAGGATGACG 660


RESULT 6
UBA309645
LOCUS       UBA309645                902 bp    DNA     linear   BCT 06-JUN-2003
DEFINITION  Uncultured Chloroflexaceae group bacterium 16S rRNA gene, clone
            P6-C03.
ACCESSION   AJ309645
VERSION     AJ309645.1  GI:15552891
KEYWORDS    16S ribosomal RNA; 16S rRNA gene.
SOURCE      uncultured Chloroflexales bacterium
  ORGANISM  uncultured Chloroflexales bacterium
            Bacteria; Chloroflexi; Chloroflexales; environmental samples.
REFERENCE   1  (bases 1 to 902)
  AUTHORS   Nubel,U., Bateson,M.M., Madigan,M.T., Kuhl,M. and Ward,D.M.
  TITLE     Diversity and distribution in hypersaline microbial mats of
            bacteria related to Chloroflexus spp
  JOURNAL   Appl. Environ. Microbiol. 67 (9), 4365-4371 (2001)
  MEDLINE   21417071
   PUBMED   11526049
REFERENCE   2  (bases 1 to 902)
  AUTHORS   Nuebel,U.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-FEB-2001) Nuebel U., Molekulare Systematik und
            Oekologie, Deutsche Sammlung von Mikroorganismen und Zellkulturen,
            Mascheroder Weg 1B, Braunschweig, 38124, GERMANY
FEATURES             Location/Qualifiers
     source          1. .902
                     /organism="uncultured Chloroflexales bacterium"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:152575"
                     /clone="P6-C03"
                     /country="Mexico"
     gene            1. .902
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     rRNA            1. .902
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                     /product="16S ribosomal RNA"
ORIGIN

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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
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Db        766 GGAGGAAGGCGAGGATGACG 785


RESULT 7
UBA309647
LOCUS       UBA309647                910 bp    DNA     linear   BCT 06-JUN-2003
DEFINITION  Uncultured Chloroflexaceae group bacterium 16S rRNA gene, clone
            P6-C12.
ACCESSION   AJ309647
VERSION     AJ309647.1  GI:15552893
KEYWORDS    16S ribosomal RNA; 16S rRNA gene.
SOURCE      uncultured Chloroflexales bacterium
  ORGANISM  uncultured Chloroflexales bacterium
            Bacteria; Chloroflexi; Chloroflexales; environmental samples.
REFERENCE   1  (bases 1 to 910)
  AUTHORS   Nubel,U., Bateson,M.M., Madigan,M.T., Kuhl,M. and Ward,D.M.
  TITLE     Diversity and distribution in hypersaline microbial mats of
            bacteria related to Chloroflexus spp
  JOURNAL   Appl. Environ. Microbiol. 67 (9), 4365-4371 (2001)
  MEDLINE   21417071
   PUBMED   11526049
REFERENCE   2  (bases 1 to 910)
  AUTHORS   Nuebel,U.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-FEB-2001) Nuebel U., Molekulare Systematik und
            Oekologie, Deutsche Sammlung von Mikroorganismen und Zellkulturen,
            Mascheroder Weg 1B, Braunschweig, 38124, GERMANY
FEATURES             Location/Qualifiers
     source          1. .910
                     /organism="uncultured Chloroflexales bacterium"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:152575"
                     /clone="P6-C12"
                     /country="Mexico"
     gene            1. .910
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     rRNA            1. .910
                     /gene="16S rRNA"
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ORIGIN

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Qy          1 GGAGGAAGGCGAGGATGACG 20
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Db        780 GGAGGAAGGCGAGGATGACG 799


RESULT 8
UBA309611
LOCUS       UBA309611                911 bp    DNA     linear   BCT 06-JUN-2003
DEFINITION  Uncultured Chloroflexaceae group bacterium 16S rRNA gene, clone
            P4-D01.
ACCESSION   AJ309611
VERSION     AJ309611.1  GI:15552857
KEYWORDS    16S ribosomal RNA; 16S rRNA gene.
SOURCE      uncultured Chloroflexales bacterium
  ORGANISM  uncultured Chloroflexales bacterium
            Bacteria; Chloroflexi; Chloroflexales; environmental samples.
REFERENCE   1  (bases 1 to 911)
  AUTHORS   Nubel,U., Bateson,M.M., Madigan,M.T., Kuhl,M. and Ward,D.M.
  TITLE     Diversity and distribution in hypersaline microbial mats of
            bacteria related to Chloroflexus spp
  JOURNAL   Appl. Environ. Microbiol. 67 (9), 4365-4371 (2001)
  MEDLINE   21417071
   PUBMED   11526049
REFERENCE   2  (bases 1 to 911)
  AUTHORS   Nuebel,U.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-FEB-2001) Nuebel U., Molekulare Systematik und
            Oekologie, Deutsche Sammlung von Mikroorganismen und Zellkulturen,
            Mascheroder Weg 1B, Braunschweig, 38124, GERMANY
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:152575"
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ORIGIN

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Qy          1 GGAGGAAGGCGAGGATGACG 20
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Db        781 GGAGGAAGGCGAGGATGACG 800


RESULT 9
AF050608
LOCUS       AF050608                 936 bp    DNA     linear   BCT 15-OCT-1998
DEFINITION  Uncultured eubacterium WCHA1-16 16S ribosomal RNA gene, partial
            sequence.
ACCESSION   AF050608
VERSION     AF050608.1  GI:2967784
KEYWORDS    .
SOURCE      uncultured eubacterium WCHA1-16
  ORGANISM  uncultured eubacterium WCHA1-16
            Bacteria; candidate division OP11; environmental samples.
REFERENCE   1  (bases 1 to 936)
  AUTHORS   Dojka,M.A., Hugenholtz,P., Haack,S.K. and Pace,N.R.
  TITLE     Microbial diversity in a hydrocarbon- and
            chlorinated-solvent-contaminated aquifer undergoing intrinsic
            bioremediation
  JOURNAL   Appl. Environ. Microbiol. 64 (10), 3869-3877 (1998)
  MEDLINE   98432811
   PUBMED   9758812
REFERENCE   2  (bases 1 to 936)
  AUTHORS   Dojka,M.A. Jr., Hugenholtz,P., Haack,S. and Pace,N.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-FEB-1998) Plant and Microbial Biology, University of
            California, Berkeley, 111 Koshland Hall, Berkeley, CA 94720, USA
FEATURES             Location/Qualifiers
     source          1. .936
                     /organism="uncultured eubacterium WCHA1-16"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:74258"
                     /clone="WCHA1-16"
                     /note="isolated from a contaminated aquifer"
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ORIGIN

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Qy          1 GGAGGAAGGCGAGGATGACG 20
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Db        629 GGAGGAAGGCGAGGATGACG 648


RESULT 10
UBA519648
LOCUS       UBA519648               1247 bp    rRNA    linear   BCT 29-NOV-2002
DEFINITION  Uncultured bacterium partial 16S rRNA gene, clone Sh765B-AG-14.
ACCESSION   AJ519648
VERSION     AJ519648.1  GI:26005694
KEYWORDS    16S ribosomal RNA; 16S rRNA gene.
SOURCE      uncultured bacterium
  ORGANISM  uncultured bacterium
            Bacteria; environmental samples.
REFERENCE   1
  AUTHORS   Geissler,A.
  TITLE     Bakterielle Diversitaet in Erdproben aus Uranabfallhalden
  JOURNAL   Unpublished
REFERENCE   2
  AUTHORS   Geissler,A., Tzvetkova,T., Flemming,K. and Selenska-Pobell,S.
  TITLE     Comparison of natural bacterial communities found in uranium mining
            waste piles and mill tailings
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1247)
  AUTHORS   Selenska-Pobell,S.I.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-NOV-2002) Selenska-Pobell S.I., Molecular
            Microbiology, Institute of Radiochemistry, FZR, P.O.B. 51 01 19,
            D-01314 Dresden, GERMANY
FEATURES             Location/Qualifiers
     source          1. .1247
                     /organism="uncultured bacterium"
                     /mol_type="rRNA"
                     /isolation_source="uranium mill tailings, soil sample"
                     /db_xref="taxon:77133"
                     /clone="Sh765B-AG-14"
                     /clone_lib="43F-1404R"
                     /environmental_sample
                     /country="USA:Shiprock, New Mexico"
     gene            1. .1247
                     /gene="16S rRNA"
     rRNA            <1. .>1247
                     /gene="16S rRNA"
                     /product="16S ribosomal RNA"
ORIGIN

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Db       1048 GGAGGAAGGCGAGGATGACG 1067
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RESULT 11
AF524023
LOCUS       AF524023               1255 bp    DNA     linear   BCT 26-DEC-2002
DEFINITION  Uncultured bacterium clone FW128 16S ribosomal RNA gene, partial
            sequence.
ACCESSION   AF524023
VERSION     AF524023.1  GI:21952426
KEYWORDS    .
SOURCE      uncultured bacterium
  ORGANISM  uncultured bacterium
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 1255)
  AUTHORS   Brofft,J.E., McArthur,J.V. and Shimkets,L.J.
  TITLE     Recovery of novel bacterial diversity from a forested wetland
            impacted by reject coal
  JOURNAL   Environ. Microbiol. 4 (11), 764-769 (2002)
  MEDLINE   22349383
   PUBMED   12460285
REFERENCE   2  (bases 1 to 1255)
  AUTHORS   Brofft,J.E., Shimkets,L.J. and McArthur,J.V.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2002) Microbiology, University of Georgia, 527
            Biological Sciences, Athens, GA 30602, USA
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /isolation_source="forested wetland"
                     /db_xref="taxon:77133"
                     /clone="FW128"
                     /environmental_sample
     rRNA            <1. .>1255
                     /product="16S ribosomal RNA"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 32;
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Qy          1 GGAGGAAGGCGAGGATGACG 20
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Db       1076 GGAGGAAGGCGAGGATGACG 1095


RESULT 12
APBRGDC
LOCUS       APBRGDC                1298 bp    DNA     linear   BCT 13-SEP-2002
DEFINITION  Alpha proteobacterium sp. (clone SAR102) 16S ribosomal RNA (16S
            rRNA) gene, complete rRNA.
ACCESSION   L35460
VERSION     L35460.1  GI:529971
KEYWORDS    16S ribosomal RNA.
SOURCE      uncultured alpha proteobacterium
  ORGANISM  uncultured alpha proteobacterium
            Bacteria; Proteobacteria; Alphaproteobacteria; environmental
            samples.
REFERENCE   1  (bases 1 to 1298)
  AUTHORS   Mullins,T.D., Britschgi,T.B., Krest,R.L. and Giovannoni,S.J.
  TITLE     Genetic comparisons reveal the same unknown bacterial lineages in
            Atlantic and Pacific Bacterioplankton communities
  JOURNAL   Limnol. Oceanogr. 40 (1), 147-158 (1995)
COMMENT     Original source text: Alpha proteobacterium sp (clone: SAR102) DNA.
FEATURES             Location/Qualifiers
     source          1. .1298
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                     /db_xref="taxon:91750"
                     /clone="SAR102"
     gene            1. .1298
                     /gene="16S rRNA"
     rRNA            1. .1298
                     /gene="16S rRNA"
                     /product="16S ribosomal RNA"
ORIGIN

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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
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Db       1067 GGAGGAAGGCGAGGATGACG 1086


RESULT 13
AB088955
LOCUS       AB088955               1313 bp    DNA     linear   BCT 26-APR-2003
DEFINITION  Uncultured Eubacteriaceae bacterium gene for 16S rRNA, partial
            sequence, clone:Rs-M13.
ACCESSION   AB088955
VERSION     AB088955.1  GI:27530167
KEYWORDS    .
SOURCE      uncultured Eubacteriaceae bacterium
  ORGANISM  uncultured Eubacteriaceae bacterium
            Bacteria; Firmicutes; Clostridia; Clostridiales; Eubacteriaceae;
            environmental samples.
REFERENCE   1
  AUTHORS   Hongoh,Y., Ohkuma,M. and Kudo,T.
  TITLE     Molecular analysis of bacterial microbiota in the gut of the
            termite Reticulitermes speratus (Isoptera; Rhinotermitidae)
  JOURNAL   FEMS Microbiol. Ecol. 44, 231-242 (2003)
REFERENCE   2  (bases 1 to 1313)
  AUTHORS   Hongoh,Y., Ohkuma,M. and Kudo,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-JUL-2002) Yuichi Hongoh, Japan Science and Technology
            Corporation (JST), Bio-Recycle Project, International Cooperative
            Research Project; Hirosawa 2-1, Wako-shi, Saitama 351-0198, Japan
            (E-mail:yhongo@postman.riken.go.jp, Tel:81-48-467-9546,
            Fax:81-48-462-4672)
FEATURES             Location/Qualifiers
     source          1. .1313
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                     /mol_type="genomic DNA"
                     /isolation_source="PCR-derived sequence from termite gut
                     homogenate"
                     /specific_host="Reticulitermes speratus"
                     /db_xref="taxon:203524"
                     /clone="Rs-M13"
                     /environmental_sample
                     /country="Japan:Saitama, Ogose"
     rRNA            <1. .>1313
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGAGGAAGGCGAGGATGACG 20
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Db       1099 GGAGGAAGGCGAGGATGACG 1118


RESULT 14
AF229791
LOCUS       AF229791               1318 bp    DNA     linear   BCT 01-FEB-2001
DEFINITION  Uncultured bacterium TA18 16S ribosomal RNA gene, partial sequence.
ACCESSION   AF229791
VERSION     AF229791.1  GI:12642398
KEYWORDS    .
SOURCE      uncultured bacterium TA18
  ORGANISM  uncultured bacterium TA18
            Bacteria; environmental samples.
REFERENCE   1  (bases 1 to 1318)
  AUTHORS   Wu,J.H., Liu,W.T., Tseng,I.C. and Cheng,S.S.
  TITLE     Characterization of microbial consortia in a
```

terephthalate-degrading anaerobic granular sludge system
JOURNAL Microbiology 147 (Pt 2), 373-382 (2001)
MEDLINE 21097276
PUBMED 11158354
REFERENCE 2 (bases 1 to 1318)
AUTHORS Wu,J.H., Liu,W.T., Tseng,I.C. and Cheng,S.S.
TITLE Direct Submission
JOURNAL Submitted (01-FEB-2000) Department of Environmental Engineering, National Cheng Kung University, 1 University Road, Tainan 701, Taiwan, ROC
FEATURES Location/Qualifiers
source 1. .1318
/organism="uncultured bacterium TA18"
/mol_type="genomic DNA"
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/clone="TA18"
rRNA <1. .>1318
/product="16S ribosomal RNA"
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGAAGGCGAGGATGACG 20
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Db 1026 GGAGGAAGGCGAGGATGACG 1045

RESULT 15
AF127027
LOCUS AF127027 1335 bp DNA linear BCT 17-NOV-1999
DEFINITION Helicobacter bovis 16S ribosomal RNA gene, partial sequence.
ACCESSION AF127027
VERSION AF127027.1 GI:6018194
KEYWORDS .
SOURCE Candidatus Helicobacter bovis
ORGANISM Candidatus Helicobacter bovis
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter.
REFERENCE 1 (bases 1 to 1335)
AUTHORS De Groote,D., van Doorn,L.J., Ducatelle,R., Verschuuren,A., Tilmant,K., Quint,W.G., Haesebrouck,F. and Vandamme,P.
TITLE Phylogenetic characterization of 'Candidatus Helicobacter bovis', a new gastric helicobacter in cattle
JOURNAL Int. J. Syst. Bacteriol. 49 Pt 4, 1707-1715 (1999)
MEDLINE 20023052
PUBMED 10555352
REFERENCE 2 (bases 1 to 1335)
AUTHORS De Groote,D., van Doorn,L.-J., Ducatelle,R., Verschuuren,A., Tilmant,K., Haesebrouck,F., Quint,W. and Vandamme,P.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1999) Pathology, Bacteriology and Avian Diseases, University Ghent, Salisburylaan 133, Merelbeke B-9820, Belgium
FEATURES Location/Qualifiers
source 1. .1335
/organism="Candidatus Helicobacter bovis"
/mol_type="genomic DNA"
/specific_host="Bos taurus"
/db_xref="taxon:104629"
/clone="R2XA"
/note="from bovine abomasum"
rRNA <1. .>1335
/product="16S ribosomal RNA"
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 1335;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1103 GGAGGAAGGCGAGGATGACG 1122

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OM nucleic - nucleic search, using sw model

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Scoring table: OLIGO_NUC
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Searched: 3470272 seqs, 21671516995 residues

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Post-processing: Listing first 45 summaries

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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		20	100.0	23	6	AX575427	AX575427 Sequence
2		20	100.0	37	6	AX709025	AX709025 Sequence
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4		20	100.0	129	1	MCO16SR2	D11230 Marinomonas
5		20	100.0	131	1	LPNRRDA02	M19442 L.pneumophi
6		20	100.0	131	1	TAMRRD01	M19451 T.micdadei
7		20	100.0	131	1	TAMRRDB02	M19446 T.micdadei
8		20	100.0	131	1	VIB16SR11	D11247 Vibrio chol
9		20	100.0	133	1	TAMRRDA02	M19449 T.micdadei
10		20	100.0	137	1	CLO16SRNAA	M98449 Clostridium
11		20	100.0	137	1	LPNRRDC02	M19444 L.pneumophi
12		20	100.0	137	6	E05154	E05154 Sequence of
13		20	100.0	138	1	CLORDNA16S	L08598 Clostridium
14		20	100.0	140	1	LPNBMRRN02	M24643 F.bozemanae
15		20	100.0	140	1	LPNDTRRN02	M24642 F.dumoffii
16		20	100.0	150	1	ALTE16SR2	D11220 Alteromonas
17		20	100.0	150	1	VIB16SR12	D11248 Vibrio chol
18		20	100.0	155	1	AEOS16SR	D11224 Aeromonas s
19		20	100.0	161	6	E05163	E05163 Sequence of
20		20	100.0	164	1	TAMRRN02	M34713 T.maceacher
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23		20	100.0	176	1	D28574S2	D28575 Sphingomona
24		20	100.0	176	1	VIB16SR10	D11246 Vibrio chol
25		20	100.0	178	1	PHRL16SR	D11233 Photobacter
26		20	100.0	182	1	AEOH16SR2	D11219 Aeromonas h
27		20	100.0	183	1	UOU46521	U46521 Unidentifie
28	c	20	100.0	188	1	AY373834	AY373834 Unculture
29	c	20	100.0	189	1	AY373835	AY373835 Unculture
30		20	100.0	191	1	VIB16SR20	D11256 Vibrio loge
31		20	100.0	191	6	AX575429	AX575429 Sequence
32		20	100.0	192	1	AF045813	AF045813 Unculture
33		20	100.0	193	1	AF228141	AF228141 Marine se
34		20	100.0	193	1	AF228146	AF228146 Marine se
35	c	20	100.0	195	6	I28355	I28355 Sequence 7
36	c	20	100.0	195	6	BD011645	BD011645 DNA oligo
37		20	100.0	196	1	AF045815	AF045815 Unculture
38		20	100.0	200	1	AF045823	AF045823 Unculture
39		20	100.0	200	1	UBA421167	AJ421167 Unculture
40	c	20	100.0	200	1	UEU405022	AJ405022 unculture
41		20	100.0	203	1	AF045827	AF045827 Unculture
42		20	100.0	206	1	ALTH16SR2	D11221 Alteromonas
43		20	100.0	207	1	AEOM16SR	D11223 Aeromonas m
44		20	100.0	207	1	LAEP16SR2	D11229 Listonella
45		20	100.0	207	1	VIB16SR13	D11249 Vibrio cost

ALIGNMENTS

RESULT 1
AX575427
LOCUS AX575427 23 bp DNA linear PAT 07-JAN-2003
DEFINITION Sequence 2 from Patent WO02077271.
ACCESSION AX575427
VERSION AX575427.1 GI:27552061
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Vollenbroich,D. and Schramm,C.
TITLE Control plasmid and method for detecting mycoplasma contamination in biological material
JOURNAL Patent: WO 02077271-A 2 03-OCT-2002;

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            Minerva Biolabs GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"
                     /note="Primer"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
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Db          4 GCAAACAGGATTAGATACCC 23


RESULT 2
AX709025
LOCUS       AX709025                  37 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 1 from Patent WO03014382.
ACCESSION   AX709025
VERSION     AX709025.1  GI:29564699
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mittermayr,C.R., Ronacher,B., Winner,F. and Zehethofer,K.
  TITLE     Device for analyzing nucleic acid
  JOURNAL   Patent: WO 03014382-A 1 20-FEB-2003;
            Lambda Labor fuer Molekularbiologische DNA-Analysen GmbH (AT)
FEATURES             Location/Qualifiers
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                     /note="Primer"
ORIGIN

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Qy          1 GCAAACAGGATTAGATACCC 20
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Db          6 GCAAACAGGATTAGATACCC 25


RESULT 3
BD140316/c
LOCUS       BD140316                  47 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Universal eubacteria nucleic acid probe and method.
ACCESSION   BD140316
VERSION     BD140316.1  GI:23235261
KEYWORDS    JP 2002051799-A/9.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Lane,D.J., Shah,J., Buharin,A. and Weisburg,W.G.
  TITLE     Universal eubacteria nucleic acid probe and method
  JOURNAL   Patent: JP 2002051799-A 9 19-FEB-2002;
            GENE TRAK SYSTEMS
COMMENT     OS   Artificial Sequence
            PN   JP 2002051799-A/9
            PD   19-FEB-2002
            PF   11-APR-2001 JP 2001150160
            PR   31-MAY-1989 US       359158
            PI   DAVID J LANE,JYOTSNA SHAH,AMELIA BUHARIN,WILLIAM G WEISBURG PC
              C12Q1/68,C12N15/09,C12N15/09,C12N15/00,C12N15/00 CC   Synthesized
            probe for hybridization
            FH   Key             Location/Qualifiers
            FT   source          1. .47
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
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ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 47;
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         33 GCAAACAGGATTAGATACCC 14


RESULT 4
MCO16SR2
LOCUS       MCO16SR2                 129 bp    rRNA    linear   BCT 04-NOV-1999
DEFINITION  Marinomonas communis 16S rRNA.
ACCESSION   D11230
VERSION     D11230.1  GI:286047
KEYWORDS    .
SOURCE      Marinomonas communis
  ORGANISM  Marinomonas communis
            Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
            Marinomonas.
REFERENCE   1  (bases 1 to 129)
  AUTHORS   Kita-Tsukamoto,K., Oyaizu,H., Nanba,K. and Simidu,U.
  TITLE     Phylogenetic relationships of marine bacteria, mainly members of
            the family Vibrionaceae, determined on the basis of 16S rRNA
            sequences
  JOURNAL   Int. J. Syst. Bacteriol. 43 (1), 8-19 (1993)
  MEDLINE   93152464
   PUBMED   8427811
REFERENCE   2  (bases 1 to 129)
  AUTHORS   Kita-Tsukamoto,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-1992) Kumiko Kita-Tsukamoto, University of Tokyo,
            Ocean Research Institute; 1-15-1 Minamidai, Nakano-ku, Tokyo 164,
            Japan (E-mail:tukamoto@aix3.ori.u-tokyo.ac.jp, Tel:03-3376-1251,
            Fax:03-3375-6716)
FEATURES             Location/Qualifiers
     source          1. .129
                     /organism="Marinomonas communis"
                     /mol_type="rRNA"
                     /strain="IAM12914"
                     /db_xref="taxon:28254"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 1;  Length 129;
  Best Local Similarity   100.0%;  Pred. No. 6e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db          4 GCAAACAGGATTAGATACCC 23


RESULT 5
LPNRRDA02
LOCUS       LPNRRDA02                131 bp    rRNA    linear   BCT 23-JUL-1993
DEFINITION  L.pneumophila (strain Chicago-2) 16S rRNA, partial, segment 2 of 3.
ACCESSION   M19442
VERSION     M19442.1  GI:175170
KEYWORDS    16S ribosomal RNA.
SEGMENT     2 of 3
SOURCE      Legionella pneumophila
  ORGANISM  Legionella pneumophila
            Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
```

```
            Legionellaceae; Legionella.
REFERENCE   1  (bases 1 to 131)
  AUTHORS   Fox,K., Brown,A. and Schnitzer,G.
  TITLE     Partial sequence analysis of the 16s-rRNA of Legionellae: Taxonomic
            implications
  JOURNAL   Syst. Appl. Microbiol. 11, 135-139 (1989)
REFERENCE   2  (sites)
  AUTHORS   Brown,A., Fox,K.F. and Schnitzer,G.
  TITLE     Tatlockia, a genetically and chemically distinct group of bacteria:
            Proposal to transfer Legionella maceachernii (Brenner, et al.) to
            the genus Tatlockia as Tatlockia maceachernii comb. nov
  JOURNAL   Syst. Appl. Microbiol. 14, 52-56 (1991)
COMMENT     Original source text: L.pneumophila (ATCC 33215; strain Chicago-2)
            ribosomal RNA.
FEATURES             Location/Qualifiers
     source          1. .131
                     /organism="Legionella pneumophila"
                     /mol_type="rRNA"
                     /db_xref="taxon:446"
     rRNA            <1. .>131
                     /product="16S ribosomal RNA"
ORIGIN      About 250 bp after segment 1.

  Query Match            100.0%;  Score 20;  DB 1;  Length 131;
  Best Local Similarity  100.0%;  Pred. No. 5.9e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db          4 GCAAACAGGATTAGATACCC 23


RESULT 6
TAMRRD01
LOCUS       TAMRRD01                131 bp    rRNA    linear   BCT 23-JUL-1993
DEFINITION  T.micdadei (strain PPA-JC) 16S rRNA, partial, segment 1 of 3.
ACCESSION   M19451
VERSION     M19451.1  GI:176096
KEYWORDS    16S ribosomal RNA.
SEGMENT     1 of 3
SOURCE      Tatlockia micdadei
  ORGANISM  Tatlockia micdadei
            Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
            Legionellaceae; Tatlockia.
REFERENCE   1  (bases 1 to 131)
  AUTHORS   Fox,K., Brown,A. and Schnitzer,G.
  TITLE     Partial sequence analysis of the 16s-rRNA of Legionellae: Taxonomic
            implications
  JOURNAL   Syst. Appl. Microbiol. 11, 135-139 (1989)
REFERENCE   2  (sites)
  AUTHORS   Brown,A., Fox,K.F. and Schnitzer,G.
  TITLE     Tatlockia, a genetically and chemically distinct group of bacteria:
            Proposal to transfer Legionella maceachernii (Brenner, et al.) to
            the genus Tatlockia as Tatlockia maceachernii comb. nov
  JOURNAL   Syst. Appl. Microbiol. 14, 52-56 (1991)
COMMENT     Original source text: T.micdadei (strain PPA-JC) ribosomal RNA.
FEATURES             Location/Qualifiers
     source          1. .131
                     /organism="Tatlockia micdadei"
                     /mol_type="rRNA"
                     /db_xref="taxon:451"
     rRNA            <1. .>131
                     /product="16S ribosomal RNA"
ORIGIN

  Query Match            100.0%;  Score 20;  DB 1;  Length 131;
  Best Local Similarity  100.0%;  Pred. No. 5.9e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db          4 GCAAACAGGATTAGATACCC 23


RESULT 7
TAMRRDB02
LOCUS       TAMRRDB02               131 bp    rRNA    linear   BCT 23-JUL-1993
DEFINITION  T.micdadei (strain Pgh-12) 16S rRNA, partial, segment 2 of 3.
ACCESSION   M19446
VERSION     M19446.1  GI:176105
KEYWORDS    16S ribosomal RNA.
SEGMENT     2 of 3
SOURCE      Tatlockia micdadei
  ORGANISM  Tatlockia micdadei
            Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
            Legionellaceae; Tatlockia.
REFERENCE   1  (bases 1 to 131)
  AUTHORS   Fox,K., Brown,A. and Schnitzer,G.
  TITLE     Partial sequence analysis of the 16s-rRNA of Legionellae: Taxonomic
            implications
  JOURNAL   Syst. Appl. Microbiol. 11, 135-139 (1989)
REFERENCE   2  (sites)
  AUTHORS   Brown,A., Fox,K.F. and Schnitzer,G.
  TITLE     Tatlockia, a genetically and chemically distinct group of bacteria:
            Proposal to transfer Legionella maceachernii (Brenner, et al.) to
            the genus Tatlockia as Tatlockia maceachernii comb. nov
  JOURNAL   Syst. Appl. Microbiol. 14, 52-56 (1991)
COMMENT     Original source text: T.micdadei (ATCC 33346; strain Pgh-12)
            ribosomal RNA.
FEATURES             Location/Qualifiers
     source          1. .131
                     /organism="Tatlockia micdadei"
                     /mol_type="rRNA"
                     /db_xref="taxon:451"
     rRNA            <1. .>131
                     /product="16S ribosomal RNA"
ORIGIN      About 250 bp after segment 1.

  Query Match            100.0%;  Score 20;  DB 1;  Length 131;
  Best Local Similarity  100.0%;  Pred. No. 5.9e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db          4 GCAAACAGGATTAGATACCC 23


RESULT 8
VIB16SR11
LOCUS       VIB16SR11               131 bp    rRNA    linear   BCT 04-NOV-1999
DEFINITION  Vibrio cholerae 16S rRNA.
ACCESSION   D11247
VERSION     D11247.1  GI:287488
KEYWORDS    .
SOURCE      Vibrio cholerae
  ORGANISM  Vibrio cholerae
            Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
            Vibrionaceae; Vibrio.
REFERENCE   1  (bases 1 to 131)
  AUTHORS   Kita-Tsukamoto,K., Oyaizu,H., Nanba,K. and Simidu,U.
  TITLE     Phylogenetic relationships of marine bacteria, mainly members of
            the family Vibrionaceae, determined on the basis of 16S rRNA
            sequences
  JOURNAL   Int. J. Syst. Bacteriol. 43 (1), 8-19 (1993)
  MEDLINE   93152464
   PUBMED   8427811
REFERENCE   2  (bases 1 to 131)
  AUTHORS   Kita-Tsukamoto,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-APR-1992) Kumiko Kita-Tsukamoto, University of Tokyo,
            Ocean Research Institute; 1-15-1 Minamidai, Nakano-ku, Tokyo 164,
            Japan (E-mail:tukamoto@aix3.ori.u-tokyo.ac.jp, Tel:03-3376-1251,
            Fax:03-3375-6716)
FEATURES             Location/Qualifiers
     source          1. .131
                     /organism="Vibrio cholerae"
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                     /mol_type="rRNA"
                     /strain="IID 935"
                     /db_xref="taxon:666"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 1;  Length 131;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db          6 GCAAACAGGATTAGATACCC 25


RESULT 9
TAMRRDA02
LOCUS       TAMRRDA02                133 bp    rRNA    linear   BCT 23-JUL-1993
DEFINITION  T.micdadei (strain TATLOCK) 16S rRNA, partial, segment 2 of 3.
ACCESSION   M19449
VERSION     M19449.1  GI:176101
KEYWORDS    16S ribosomal RNA.
SEGMENT     2 of 3
SOURCE      Tatlockia micdadei
  ORGANISM  Tatlockia micdadei
            Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
            Legionellaceae; Tatlockia.
REFERENCE   1  (bases 1 to 133)
  AUTHORS   Fox,K., Brown,A. and Schnitzer,G.
  TITLE     Partial sequence analysis of the 16s-rRNA of Legionellae: Taxonomic
            implications
  JOURNAL   Syst. Appl. Microbiol. 11, 135-139 (1989)
REFERENCE   2  (sites)
  AUTHORS   Brown,A., Fox,K.F. and Schnitzer,G.
  TITLE     Tatlockia, a genetically and chemically distinct group of bacteria:
            Proposal to transfer Legionella maceachernii (Brenner, et al.) to
            the genus Tatlockia as Tatlockia maceachernii comb. nov
  JOURNAL   Syst. Appl. Microbiol. 14, 52-56 (1991)
COMMENT     Original source text: T.micdadei (ATCC 33218; strain TATLOCK)
            ribosomal RNA.
FEATURES             Location/Qualifiers
     source          1. .133
                     /organism="Tatlockia micdadei"
                     /mol_type="rRNA"
                     /db_xref="taxon:451"
     rRNA            <1. .>133
                     /product="16S ribosomal RNA"
ORIGIN      About 250 bp after segment 1.

  Query Match             100.0%;  Score 20;  DB 1;  Length 133;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db          6 GCAAACAGGATTAGATACCC 25


RESULT 10
CLO16SRNAA
LOCUS       CLO16SRNAA               137 bp    DNA     linear   BCT 28-MAR-1994
DEFINITION  Clostridium sp. 16S ribosomal RNA (16S rRNA) gene, partial
            sequence.
ACCESSION   M98449
VERSION     M98449.1  GI:144701
KEYWORDS    16S ribosomal RNA.
SOURCE      Clostridium sp.
  ORGANISM  Clostridium sp.
            Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
            Clostridium.
REFERENCE   1  (bases 1 to 137)
  AUTHORS   Galindo,I., Rangel-Aldao,R. and Ramirez,J.L.
  TITLE     A combined polymerase chain reaction-colour development
            hybridization assay in a microtitre format for the detection of
            Clostridium spp
  JOURNAL   Appl. Microbiol. Biotechnol. 39 (4-5), 553-557 (1993)
  MEDLINE   93356986
   PUBMED   7763926
COMMENT     Original source text: Clostridium sp. (individual_isolate
            Maracaibo) (library: EMBL4-LBB) DNA.
FEATURES             Location/Qualifiers
     source          1. .137
                     /organism="Clostridium sp."
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:1506"
     gene            1. .137
                     /gene="16S rRNA"
     rRNA            <1. .>137
                     /gene="16S rRNA"
                     /product="16S ribosomal RNA"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 1;  Length 137;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         76 GCAAACAGGATTAGATACCC 95


RESULT 11
LPNRRDC02
LOCUS       LPNRRDC02                137 bp    rRNA    linear   BCT 23-JUL-1993
DEFINITION  L.pneumophila (strain Philadelphia-1) 16S rRNA, partial, segment 2
            of 3.
ACCESSION   M19444
VERSION     M19444.1  GI:175178
KEYWORDS    16S ribosomal RNA.
SEGMENT     2 of 3
SOURCE      Legionella pneumophila
  ORGANISM  Legionella pneumophila
            Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
            Legionellaceae; Legionella.
REFERENCE   1  (bases 1 to 137)
  AUTHORS   Fox,K., Brown,A. and Schnitzer,G.
  TITLE     Partial sequence analysis of the 16s-rRNA of Legionellae: Taxonomic
            implications
  JOURNAL   Syst. Appl. Microbiol. 11, 135-139 (1989)
REFERENCE   2  (sites)
  AUTHORS   Brown,A., Fox,K.F. and Schnitzer,G.
  TITLE     Tatlockia, a genetically and chemically distinct group of bacteria:
            Proposal to transfer Legionella maceachernii (Brenner, et al.) to
            the genus Tatlockia as Tatlockia maceachernii comb. nov
  JOURNAL   Syst. Appl. Microbiol. 14, 52-56 (1991)
COMMENT     Original source text: L.pneumophila pneumophila (ATCC 33152; strain
            'Philadelphia-1) ribosomal RNA.
FEATURES             Location/Qualifiers
     source          1. .137
                     /organism="Legionella pneumophila"
                     /mol_type="rRNA"
                     /db_xref="taxon:446"
     rRNA            <1. .>137
                     /product="16S ribosomal RNA"
ORIGIN      About 250 bp after segment 1.

  Query Match             100.0%;  Score 20;  DB 1;  Length 137;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         10 GCAAACAGGATTAGATACCC 29


RESULT 12
E05154
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LOCUS       E05154                  137 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  Sequence of a DNA fraction prepared by a restriction enzyme HAP II
            from DNA coding for E.coli 16S ribosome RNA.
ACCESSION   E05154
VERSION     E05154.1  GI:2173347
KEYWORDS    JP 1993192147-A/26.
SOURCE      Escherichia coli
  ORGANISM  Escherichia coli
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Escherichia.
REFERENCE   1  (bases 1 to 137)
  AUTHORS   Shirasu,Y.
  TITLE     METHOD FOR SPECIFYING DNA BASE SEQUENCE
  JOURNAL   Patent: JP 1993192147-A 26 03-AUG-1993;
            KIRIN BIBARETSUJI KK
COMMENT     OS   Escherichia coli
            PN   JP 1993192147-A/26
            PD   03-AUG-1993
            PF   15-NOV-1991 JP 1991300882
            PI   SHIRASU YOSHIHARU
            PC   C12N15/00,C12Q1/06,C12Q1/68;
            CC   strandedness: Double;
            CC   topology: Linear;
            CC   *source: strain=K12.
FEATURES             Location/Qualifiers
     source          1. .137
                     /organism="Escherichia coli"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:562"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 6;  Length 137;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         58 GCAAACAGGATTAGATACCC 77


RESULT 13
CLORDNA16S
LOCUS       CLORDNA16S              138 bp    DNA     linear   BCT 28-MAR-1994
DEFINITION  Clostridium butyricum 16S ribosomal DNA gene.
ACCESSION   L08598
VERSION     L08598.1  GI:144899
KEYWORDS    16S ribosomal DNA.
SOURCE      Clostridium butyricum
  ORGANISM  Clostridium butyricum
            Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
            Clostridium.
REFERENCE   1  (sites)
  AUTHORS   Galindo,I., Rangel-Aldao,R. and Ramirez,J.L.
  TITLE     A combined polymerase chain reaction-colour development
            hybridization assay in a microtitre format for the detection of
            Clostridium spp
  JOURNAL   Appl. Microbiol. Biotechnol. 39 (4-5), 553-557 (1993)
  MEDLINE   93356986
   PUBMED   7763926
REFERENCE   2  (bases 1 to 138)
  AUTHORS   Galindo-Castro,I.F., Rangel,R. and Ramirez,J.L.
  TITLE     (no title given)
  JOURNAL   Unpublished (1993)
COMMENT     Original source text: Clostridium butyricum (individual_isolate Los
            Cortijos) (library: EMBL4-LBB) DNA.
FEATURES             Location/Qualifiers
     source          1. .138
                     /organism="Clostridium butyricum"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:1492"
     rRNA            1. .138
                     /product="16S ribosomal RNA"
                     /note="corresponds to position 703 of the E. coli 16S
                     ribosomal DNA gene"
ORIGIN

  Query Match             100.0%;  Score 20;  DB 1;  Length 138;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         77 GCAAACAGGATTAGATACCC 96


RESULT 14
LPNBMRRN02
LOCUS       LPNBMRRN02              140 bp    rRNA    linear   BCT 23-JUL-1993
DEFINITION  F.bozemanae (Legionella) 16S ribosomal RNA.
ACCESSION   M24643
VERSION     M24643.1  GI:175149
KEYWORDS    16S ribosomal RNA; ribosomal RNA small subunit.
SEGMENT     2 of 3
SOURCE      Fluoribacter bozemanae
  ORGANISM  Fluoribacter bozemanae
            Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
            Legionellaceae; Fluoribacter.
REFERENCE   1  (sites)
  AUTHORS   Fox,K., Brown,A. and Schnitzer,G.
  TITLE     Partial sequence analysis of the 16s-rRNA of Legionellae: Taxonomic
            implications
  JOURNAL   Syst. Appl. Microbiol. 11, 135-139 (1989)
REFERENCE   2  (bases 1 to 140)
  AUTHORS   Brown,A., Fox,K.F. and Schnitzer,G.
  TITLE     Tatlockia, a genetically and chemically distinct group of bacteria:
            Proposal to transfer Legionella maceachernii (Brenner, et al.) to
            the genus Tatlockia as Tatlockia maceachernii comb. nov
  JOURNAL   Syst. Appl. Microbiol. 14, 52-56 (1991)
COMMENT     Original source text: Fluoribacter bozemanae (strain MI-15) rRNA.
FEATURES             Location/Qualifiers
     source          1. .140
                     /organism="Fluoribacter bozemanae"
                     /mol_type="rRNA"
                     /strain="MI-15"
                     /db_xref="taxon:447"
     rRNA            <1. .>140
                     /product="16S ribosomal RNA"
ORIGIN      About 243 bp after segment 1.

  Query Match             100.0%;  Score 20;  DB 1;  Length 140;
  Best Local Similarity   100.0%;  Pred. No. 5.7e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         15 GCAAACAGGATTAGATACCC 34


RESULT 15
LPNDTRRN02
LOCUS       LPNDTRRN02              140 bp    rRNA    linear   BCT 23-JUL-1993
DEFINITION  F.dumoffii (Legionella) 16S ribosomal RNA.
ACCESSION   M24642
VERSION     M24642.1  GI:175161
KEYWORDS    16S ribosomal RNA; ribosomal RNA small subunit.
SEGMENT     2 of 3
SOURCE      Fluoribacter dumoffii
  ORGANISM  Fluoribacter dumoffii
            Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
            Legionellaceae; Fluoribacter.
REFERENCE   1  (sites)
  AUTHORS   Fox,K., Brown,A. and Schnitzer,G.
  TITLE     Partial sequence analysis of the 16s-rRNA of Legionellae: Taxonomic
            implications
  JOURNAL   Syst. Appl. Microbiol. 11, 135-139 (1989)
REFERENCE   2  (bases 1 to 140)
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```
  AUTHORS   Brown,A., Fox,K.F. and Schnitzer,G.
  TITLE     Tatlockia, a genetically and chemically distinct group of bacteria:
            Proposal to transfer Legionella maceachernii (Brenner, et al.) to
            the genus Tatlockia as Tatlockia maceachernii comb. nov
  JOURNAL   Syst. Appl. Microbiol. 14, 52-56 (1991)
COMMENT     Original source text: F.(Legionella) dumoffii (strain Tex-KL)
            ribosomal RNA.
FEATURES             Location/Qualifiers
     source          1. .140
                     /organism="Fluoribacter dumoffii"
                     /mol_type="rRNA"
                     /db_xref="taxon:463"
     rRNA            <1. .>140
                     /note="16S rRNA segment"
ORIGIN      About 243 bases after segment 1.

  Query Match           100.0%;  Score 20;  DB 1;  Length 140;
  Best Local Similarity  100.0%;  Pred. No. 5.7e+04;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         15 GCAAACAGGATTAGATACCC 34


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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 04:00:30 ; Search time 164.337 Seconds
(without alignments)
517.009 Million cell updates/sec

Title: US-09-940-860-1
Perfect score: 20
Sequence: 1 gcaaacaggattagataccc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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1: geneseqn1980s:*
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5: geneseqn2001bs:*
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9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	23	7	ABV74328	Abv74328 Mycoplasm
	2	20	100.0	24	3	AAA39031	Aaa39031 Unknown b
	3	20	100.0	37	8	ABX94830	Abx94830 16S rRNA
	4	20	100.0	37	8	ABX94859	Abx94859 16S rRNA
c	5	20	100.0	47	2	AAQ10118	Aaq10118 Probe 173
	6	20	100.0	50	6	ABL59813	Abl59813 Enterococ
	7	20	100.0	50	6	ABL59817	Abl59817 Peptostre
	8	20	100.0	50	6	ABL59820	Abl59820 Chlamydia
	9	20	100.0	50	6	ABL59819	Abl59819 Fusobacte
	10	20	100.0	50	6	ABL59786	Abl59786 Campyloba
	11	20	100.0	50	6	ABL59805	Abl59805 Myxococcu
	12	20	100.0	50	6	ABL59787	Abl59787 Helicobac
	13	20	100.0	50	6	ABL59796	Abl59796 Salmonell
	14	20	100.0	50	6	ABL59799	Abl59799 Legionell
	15	20	100.0	50	6	ABL59801	Abl59801 Caulobact
	16	20	100.0	50	6	ABL59794	Abl59794 Haemophil
	17	20	100.0	50	6	ABL59795	Abl59795 Escherich
	18	20	100.0	50	6	ABL59812	Abl59812 Listeria
	19	20	100.0	50	6	ABL59816	Abl59816 Clostridi
	20	20	100.0	50	6	ABL59804	Abl59804 Wolbachia
	21	20	100.0	50	6	ABL59790	Abl59790 Leptothri
	22	20	100.0	50	6	ABL59788	Abl59788 Treponema
	23	20	100.0	50	6	ABL59803	Abl59803 Nitrobact
	24	20	100.0	50	6	ABL59792	Abl59792 Neisseria
	25	20	100.0	50	6	ABL59791	Abl59791 Thiomicro
	26	20	100.0	50	6	ABL59802	Abl59802 Rhodospir
	27	20	100.0	50	6	ABL59793	Abl59793 Actinobac
	28	20	100.0	50	6	ABL59797	Abl59797 Vibrio ch
	29	20	100.0	50	6	ABL59800	Abl59800 Pseudomon
	30	20	100.0	105	6	ABN66212	Abn66212 Streptoco
c	31	20	100.0	122	7	ACD97427	Acd97427 Human col
	32	20	100.0	191	7	ABV74330	Abv74330 Mycoplasm
c	33	20	100.0	195	2	AAQ20319	Aaq20319 Region of
c	34	20	100.0	195	4	AAH27463	Aah27463 Polynucle
c	35	20	100.0	279	9	ADC93544	Adc93544 E. faeciu
c	36	20	100.0	279	9	ADC93543	Adc93543 E. faeciu
c	37	20	100.0	312	7	ACD92910	Acd92910 Human col
c	38	20	100.0	312	7	ACD92986	Acd92986 Human col
c	39	20	100.0	312	7	ACD93011	Acd93011 Human col
c	40	20	100.0	312	7	ACD92911	Acd92911 Human col
	41	20	100.0	338	7	ACD92089	Acd92089 Human col
	42	20	100.0	368	7	ACD92108	Acd92108 Human col
	43	20	100.0	442	3	AAC09938	Aac09938 Human sec
	44	20	100.0	549	3	AAC95222	Aac95222 Cat flea
	45	20	100.0	571	3	AAZ80671	Aaz80671 Human col

ALIGNMENTS

RESULT 1
ABV74328
ID ABV74328 standard; DNA; 23 BP.
XX
AC ABV74328;
XX
DT 29-JAN-2003 (first entry)
XX
DE Mycoplasma 16S rRNA gene PCR primer SEQ ID NO 2.
XX
KW Mollicutes sp; Mycoplasma; 16S rRNA; infection; PCR; primer; ss.
XX
OS Mycoplasma sp.
XX
PN WO200277271-A2.
XX
PD 03-OCT-2002.
XX
PF 25-MAR-2002; 2002WO-DE001154.
XX
PR 25-MAR-2001; 2001DE-01015749.
XX
PA (MINE-) MINERVA BIOLABS GMBH.
XX
PI Vollenbroich D, Schramm C;
XX
DR WPI; 2003-040591/03.
XX
PT Control plasmid, useful as internal standard in amplification method for
PT detecting Mycoplasma, contains primers that recognize parts of the
PT Mycoplasma 16S rRNA gene.
XX
PS Claim 2; Page 15; 25pp; German.
XX
CC The invention relates to a control plasmid (A) containing: (a) primers
CC that recognize a segment of the 16S rRNA-encoding gene in the Mycoplasma
CC genome; and (b) between the primers an amplicon that includes the
CC sequence (i). (A) is used as a control in a PCR method for detecting
CC Mycoplasma in biological materials, e.g. for diagnosing infections or
CC detecting contamination of cell cultures. (A) provides an internal
CC control for PCR detection of Mycoplasma to exclude false negatives. The
CC method is more sensitive and specific than known processes, providing
CC reliable detection of even very low titers of Mycoplasma and when used in
CC real-time PCR, has a broad dynamic and linear measurement range, allowing
CC accurate quantitation. The present sequence is that of a Mycoplasma 16S
CC rRNA gene PCR primer of the invention

XX
SQ Sequence 23 BP; 9 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 7; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 4 GCAAACAGGATTAGATACCC 23

RESULT 2
AAA39031
ID AAA39031 standard; DNA; 24 BP.
XX
AC AAA39031;
XX
DT 25-AUG-2000 (first entry)
XX
DE Unknown bacterial 16S rRNA gene primer 0776F SEQ ID NO:9.
XX
KW Bacterial; 16S rRNA; identification; polymorphism; microorganism;
KW classification; primer; human medicine; veterinary medicine; agriculture;
KW food science; industrial microbiology; infectious disease; food safety;
KW ss.
XX
OS Unidentified.
XX
PN US6054278-A.
XX
PD 25-APR-2000.
XX
PF 05-MAY-1998; 98US-00073465.
XX
PR 05-MAY-1997; 97US-0045603P.
XX
PA (PEKE) PERKIN-ELMER CORP.
XX
PI Smith DH, Dodge DE;
XX
DR WPI; 2000-338488/29.
XX
PT Identifying an unknown microorganism by generating a composite sequence
PT of its ribosomal RNA gene region and comparing with composite ribosomal
PT RNA region sequences of distinct microorganisms in a database.
XX
PS Example; Col 10; 11pp; English.
XX
CC The present invention describes a method for identifying a microorganism
CC by comparing a composite sequence (I) of a ribosomal RNA gene region with
CC rRNA region sequences of unknown microorganisms in a database and
CC identifying the region in the database that matches with (I). (I) is
CC generated by simultaneously obtaining nucleotide base sequence data from
CC every copy of the rRNA gene region in the genome of the unknown
CC microorganism. Also described is a method for identifying the species of
CC microorganism by generating (I) and entering it into a first data
CC register of a programmable computer, comparing the first data register
CC with reference data registers that encode a unique composite rRNA
CC sequence corresponding to (I) and correlated with unique microorganism
CC species name, and displaying the unique microorganism name correlated
CC with the best matching first data register. The method is useful for
CC identifying microorganisms which are useful in a variety of fields
CC including human medicine, veterinary medicine, agriculture, food science
CC and industrial microbiology. The microorganisms found in patients
CC suffering from an infectious disease can also be identified.
CC Microorganism identification is also useful for monitoring food safety by
CC testing for pathogens. Plants harbouring phytopathogenic bacteria are
CC also identified. The method is convenient and efficient as there is no
CC need to isolate one or more individual 16S rRNA genes. AAA39023 to
CC AAA39039 represent primers for the 16S rRNA gene, which are used in the
CC exemplification of the present invention
XX

SQ Sequence 24 BP; 9 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 2 GCAAACAGGATTAGATACCC 21

RESULT 3
ABX94830
ID ABX94830 standard; DNA; 37 BP.
XX
AC ABX94830;
XX
DT 11-JUL-2003 (first entry)
XX
DE 16S rRNA forward PCR primer SEQ ID 1.
XX
KW Probe; detection; primer; 16S rRNA; amplification; parodontitis; SNP;
KW gene expression pattern; single-nucleotide polymorphism; ss.
XX
OS Unidentified.
XX
PN WO2003014382-A2.
XX
PD 20-FEB-2003.
XX
PF 08-AUG-2002; 2002WO-AT000239.
XX
PR 09-AUG-2001; 2001AT-00001247.
XX
PA (LAMB-) LAMBDA LABOR MOLEKULARBIOLOGISCHE.
XX
PI Mittermayr CR, Ronacher B, Winner F, Zehethofer K;
XX
DR WPI; 2003-256597/25.
XX
PT Device for determining analytes, useful e.g. for detecting bacteria that
PT cause parodontitis, comprises a surface with immobilized analytical and
PT control agents.
XX
PS Disclosure; Page 26; 51pp; German.
XX
CC This invention describes a novel device for detecting analytes in a
CC sample. The device comprises a carrier surface which contains at least
CC one analytical region (including at least one immobilised binding partner
CC for the analyte) and at least one control region which controls of the
CC quality of analysis. The device is particularly used for nucleic acid
CC amplification and detection of (i) bacterial species associated with
CC parodontitis, (ii) gene expression patterns and (iii) single-nucleotide
CC polymorphisms (SNP's). The device provides reproducible, rapid and simple
CC analysis of nucleic acid sequences. The control system is subjected to
CC exactly the same series of operations as the analytical regions, so no
CC extra time for the control step is required and system costs are not
CC significantly more than for analysis without a control. If the device is
CC stored for archiving, the control results are also saved. Many different
CC analytes can be detected simultaneously and controls for many different
CC aspects of analytical quality can be included. This sequence represents
CC an oligonucleotide associated with the detection of 16S rRNA from various
CC bacterial samples, which is used to illustrate the device of the
CC invention
XX
SQ Sequence 37 BP; 11 A; 8 C; 12 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||

```
Db          6 GCAAACAGGATTAGATACCC 25


RESULT 4
ABX94859
ID   ABX94859 standard; DNA; 37 BP.
XX
AC   ABX94859;
XX
DT   11-JUL-2003  (first entry)
XX
DE   16S rRNA detection associated positive control oligonucleotide #3.
XX
KW   Probe; detection; primer; 16S rRNA; amplification; parodontitis; SNP;
KW   gene expression pattern; single-nucleotide polymorphism; ss.
XX
OS   Unidentified.
XX
PN   WO2003014382-A2.
XX
PD   20-FEB-2003.
XX
PF   08-AUG-2002; 2002WO-AT000239.
XX
PR   09-AUG-2001; 2001AT-00001247.
XX
PA   (LAMB-) LAMBDA LABOR MOLEKULARBIOLOGISCHE.
XX
PI   Mittermayr CR,  Ronacher B,  Winner F,  Zehethofer K;
XX
DR   WPI; 2003-256597/25.
XX
PT   Device for determining analytes, useful e.g. for detecting bacteria that
PT   cause parodontitis, comprises a surface with immobilized analytical and
PT   control agents.
XX
PS   Claim 22; Page 37; 51pp; German.
XX
CC   This invention describes a novel device for detecting analytes in a
CC   sample. The device comprises a carrier surface which contains at least
CC   one analytical region (including at least one immobilised binding partner
CC   for the analyte) and at least one control region which controls of the
CC   quality of analysis. The device is particularly used for nucleic acid
CC   amplification and detection of (i) bacterial species associated with
CC   parodontitis, (ii) gene expression patterns and (iii) single-nucleotide
CC   polymorphisms (SNP's). The device provides reproducible, rapid and simple
CC   analysis of nucleic acid sequences. The control system is subjected to
CC   exactly the same series of operations as the analytical regions, so no
CC   extra time for the control step is required and system costs are not
CC   significantly more than for analysis without a control. If the device is
CC   stored for archiving, the control results are also saved. Many different
CC   analytes can be detected simultaneously and controls for many different
CC   aspects of analytical quality can be included. This sequence represents
CC   an oligonucleotide associated with the detection of 16S rRNA from various
CC   bacterial samples, which is used to illustrate the device of the
CC   invention
XX
SQ   Sequence 37 BP; 11 A; 8 C; 12 G; 6 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 20;  DB 8;  Length 37;
  Best Local Similarity  100.0%;  Pred. No. 0.099;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db          6 GCAAACAGGATTAGATACCC 25


RESULT 5
AAQ10118/c
ID   AAQ10118 standard; DNA; 47 BP.
XX
AC   AAQ10118;
XX
DT   27-AUG-2003  (revised)
DT   09-JAN-2003  (revised)
DT   14-MAR-1991  (first entry)
XX
DE   Probe 1739 to the 16s rRNA of Eubacteria.
XX
KW   ribosomal RNA; ss.
XX
OS   Eubacteria.
XX
PN   WO9015157-A.
XX
PD   13-DEC-1990.
XX
PF   31-MAY-1989;   89US-00359158.
XX
PR   31-MAY-1989;   89US-00359158.
XX
PA   (GENE-) GENE-TRAK SYST.
XX
PI   Lane DJ,  Buharin A,  Weisburg WG;
XX
DR   WPI; 1991-007226/01.
XX
PT   Nucleic acid probes - specific for RNA of Eubacteria, for use in clinical
PT   assays.
XX
PS   Disclosure; Page 14-16; 58pp; English.
XX
CC   Probes allow assay for Eubacteria to be carried out in clinical samples
CC   such as blood or urine, in a cost effective and fast manner. The probes
CC   require only small sample sizes which may be amplified, with some of the
CC   probes suitable as primers. (Updated on 09-JAN-2003 to add missing OS
CC   field.) (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 47 BP; 6 A; 15 C; 12 G; 14 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 20;  DB 2;  Length 47;
  Best Local Similarity  100.0%;  Pred. No. 0.098;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         33 GCAAACAGGATTAGATACCC 14


RESULT 6
ABL59813
ID   ABL59813 standard; DNA; 50 BP.
XX
AC   ABL59813;
XX
DT   18-JUL-2002  (first entry)
XX
DE   Enterococcus faecalis 16S rDNA fragment #3.
XX
KW   Detection; microorganism; 16S rDNA; 16S rRNA; identification; gene;
KW   microbial encephalitis; viral encephalitis; ds.
XX
OS   Enterococcus faecalis.
XX
PN   WO200210444-A1.
XX
PD   07-FEB-2002.
XX
PF   27-JUL-2001; 2001WO-AU000933.
XX
PR   28-JUL-2000; 2000AU-00009090.
XX
PA   (UNSY ) UNIV SYDNEY.
XX
PI   Hunter N,  Jacques NA,  Martin FE,  Nadkarni MA;
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XX
DR   WPI; 2002-404428/43.
XX
PT   Polynucleotide useful as primer or probe for determining microbial
PT   content in sample, has sequence which is comprised by 16S rDNA or 16S
PT   rRNA, substantially conserved amongst two or more species of
PT   microorganism.
XX
PS   Example 12; Fig 1C; 101pp; English.
XX
CC   The present invention describes a method for determining the total
CC   microbial content in a sample, comprising amplifying a target nucleotide
CC   sequence which is substantially conserved amongst 2 or more species of
CC   microorganisms. Also describes is an isolated polynucleotide (I) or its
CC   complement having a nucleotide sequence which is comprised by 16S rDNA or
CC   16S rRNA, substantially conserved amongst two or more species of
CC   microorganism. (I) can be used: (1) as a primer or probe for determining
CC   the total microbial content in a sample; (2) as a primer or probe for
CC   identifying a microorganism by its genus in a sample; and (3) as a probe
CC   for identifying a particular microorganism or prevalence of a particular
CC   genus or species of microorganism, in a sample. (I) can also be used to
CC   identify microorganisms at the genus or species level, and as a trap for
CC   total microbial-derived target material; in assessing encephalitis and
CC   distinguishing between microbial and viral encephalitis. (I) is
CC   applicable to a range of industries including the medical, agricultural
CC   and industrial industries with specific uses including enviroprotection,
CC   bioremediation, medical diagnosis, water quality control or food quality
CC   control. (I) provides an ability to detect bacteria from samples which
CC   are difficult to cultivate and that would in all practicality remain
CC   undetected or under-estimated by viable culture count methods and enables
CC   rapid differentiation of bacteria from viral infections within the
CC   limited time constraints sometimes experienced in life-threatening
CC   clinical situations. ABL59702 to ABL59821 represent 16S rDNA fragments,
CC   and ABL59822 to ABL59830 represent primers and probes, used in the
CC   exemplification of the present invention
XX
SQ   Sequence 50 BP; 14 A; 12 C; 16 G; 8 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 20;  DB 6;  Length 50;
  Best Local Similarity  100.0%;  Pred. No. 0.098;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         16 GCAAACAGGATTAGATACCC 35


RESULT 7
ABL59817
ID   ABL59817 standard; DNA; 50 BP.
XX
AC   ABL59817;
XX
DT   18-JUL-2002  (first entry)
XX
DE   Peptostreptococcus micros 16S rDNA fragment #3.
XX
KW   Detection; microorganism; 16S rDNA; 16S rRNA; identification; gene;
KW   microbial encephalitis; viral encephalitis; ds.
XX
OS   Peptostreptococcus micros.
XX
PN   WO200210444-A1.
XX
PD   07-FEB-2002.
XX
PF   27-JUL-2001; 2001WO-AU000933.
XX
PR   28-JUL-2000; 2000AU-00009090.
XX
PA   (UNSY ) UNIV SYDNEY.
XX
PI   Hunter N,  Jacques NA,  Martin FE,  Nadkarni MA;
```

```
XX
DR   WPI; 2002-404428/43.
XX
PT   Polynucleotide useful as primer or probe for determining microbial
PT   content in sample, has sequence which is comprised by 16S rDNA or 16S
PT   rRNA, substantially conserved amongst two or more species of
PT   microorganism.
XX
PS   Example 12; Fig 1C; 101pp; English.
XX
CC   The present invention describes a method for determining the total
CC   microbial content in a sample, comprising amplifying a target nucleotide
CC   sequence which is substantially conserved amongst 2 or more species of
CC   microorganisms. Also describes is an isolated polynucleotide (I) or its
CC   complement having a nucleotide sequence which is comprised by 16S rDNA or
CC   16S rRNA, substantially conserved amongst two or more species of
CC   microorganism. (I) can be used: (1) as a primer or probe for determining
CC   the total microbial content in a sample; (2) as a primer or probe for
CC   identifying a microorganism by its genus in a sample; and (3) as a probe
CC   for identifying a particular microorganism or prevalence of a particular
CC   genus or species of microorganism, in a sample. (I) can also be used to
CC   identify microorganisms at the genus or species level, and as a trap for
CC   total microbial-derived target material; in assessing encephalitis and
CC   distinguishing between microbial and viral encephalitis. (I) is
CC   applicable to a range of industries including the medical, agricultural
CC   and industrial industries with specific uses including enviroprotection,
CC   bioremediation, medical diagnosis, water quality control or food quality
CC   control. (I) provides an ability to detect bacteria from samples which
CC   are difficult to cultivate and that would in all practicality remain
CC   undetected or under-estimated by viable culture count methods and enables
CC   rapid differentiation of bacteria from viral infections within the
CC   limited time constraints sometimes experienced in life-threatening
CC   clinical situations. ABL59702 to ABL59821 represent 16S rDNA fragments,
CC   and ABL59822 to ABL59830 represent primers and probes, used in the
CC   exemplification of the present invention
XX
SQ   Sequence 50 BP; 15 A; 12 C; 15 G; 8 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 20;  DB 6;  Length 50;
  Best Local Similarity  100.0%;  Pred. No. 0.098;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         16 GCAAACAGGATTAGATACCC 35


RESULT 8
ABL59820
ID   ABL59820 standard; DNA; 50 BP.
XX
AC   ABL59820;
XX
DT   18-JUL-2002  (first entry)
XX
DE   Chlamydia trachomatis 16S rDNA fragment #3.
XX
KW   Detection; microorganism; 16S rDNA; 16S rRNA; identification; gene;
KW   microbial encephalitis; viral encephalitis; ds.
XX
OS   Chlamydia trachomatis.
XX
PN   WO200210444-A1.
XX
PD   07-FEB-2002.
XX
PF   27-JUL-2001; 2001WO-AU000933.
XX
PR   28-JUL-2000; 2000AU-00009090.
XX
PA   (UNSY ) UNIV SYDNEY.
XX
PI   Hunter N,  Jacques NA,  Martin FE,  Nadkarni MA;
```

XX
DR WPI; 2002-404428/43.
XX
PT Polynucleotide useful as primer or probe for determining microbial
PT content in sample, has sequence which is comprised by 16S rDNA or 16S
PT rRNA, substantially conserved amongst two or more species of
PT microorganism.
XX
PS Example 12; Fig 1C; 101pp; English.
XX
CC The present invention describes a method for determining the total
CC microbial content in a sample, comprising amplifying a target nucleotide
CC sequence which is substantially conserved amongst 2 or more species of
CC microorganisms. Also describes is an isolated polynucleotide (I) or its
CC complement having a nucleotide sequence which is comprised by 16S rDNA or
CC 16S rRNA, substantially conserved amongst two or more species of
CC microorganism. (I) can be used: (1) as a primer or probe for determining
CC the total microbial content in a sample; (2) as a primer or probe for
CC identifying a microorganism by its genus in a sample; and (3) as a probe
CC for identifying a particular microorganism or prevalence of a particular
CC genus or species of microorganism, in a sample. (I) can also be used to
CC identify microorganisms at the genus or species level, and as a trap for
CC total microbial-derived target material; in assessing encephalitis and
CC distinguishing between microbial and viral encephalitis. (I) is
CC applicable to a range of industries including the medical, agricultural
CC and industrial industries with specific uses including enviroprotection,
CC bioremediation, medical diagnosis, water quality control or food quality
CC control. (I) provides an ability to detect bacteria from samples which
CC are difficult to cultivate and that would in all practicality remain
CC undetected or under-estimated by viable culture count methods and enables
CC rapid differentiation of bacteria from viral infections within the
CC limited time constraints sometimes experienced in life-threatening
CC clinical situations. ABL59702 to ABL59821 represent 16S rDNA fragments,
CC and ABL59822 to ABL59830 represent primers and probes, used in the
CC exemplification of the present invention
XX
SQ Sequence 50 BP; 15 A; 11 C; 16 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 16 GCAAACAGGATTAGATACCC 35

RESULT 9
ABL59819
ID ABL59819 standard; DNA; 50 BP.
XX
AC ABL59819;
XX
DT 18-JUL-2002 (first entry)
XX
DE Fusobacterium nucleatum 16S rDNA fragment #3.
XX
KW Detection; microorganism; 16S rDNA; 16S rRNA; identification; gene;
KW microbial encephalitis; viral encephalitis; ds.
XX
OS Fusobacterium nucleatum.
XX
PN WO200210444-A1.
XX
PD 07-FEB-2002.
XX
PF 27-JUL-2001; 2001WO-AU000933.
XX
PR 28-JUL-2000; 2000AU-00009090.
XX
PA (UNSY) UNIV SYDNEY.
XX
PI Hunter N, Jacques NA, Martin FE, Nadkarni MA;

XX
DR WPI; 2002-404428/43.
XX
PT Polynucleotide useful as primer or probe for determining microbial
PT content in sample, has sequence which is comprised by 16S rDNA or 16S
PT rRNA, substantially conserved amongst two or more species of
PT microorganism.
XX
PS Example 12; Fig 1C; 101pp; English.
XX
CC The present invention describes a method for determining the total
CC microbial content in a sample, comprising amplifying a target nucleotide
CC sequence which is substantially conserved amongst 2 or more species of
CC microorganisms. Also describes is an isolated polynucleotide (I) or its
CC complement having a nucleotide sequence which is comprised by 16S rDNA or
CC 16S rRNA, substantially conserved amongst two or more species of
CC microorganism. (I) can be used: (1) as a primer or probe for determining
CC the total microbial content in a sample; (2) as a primer or probe for
CC identifying a microorganism by its genus in a sample; and (3) as a probe
CC for identifying a particular microorganism or prevalence of a particular
CC genus or species of microorganism, in a sample. (I) can also be used to
CC identify microorganisms at the genus or species level, and as a trap for
CC total microbial-derived target material; in assessing encephalitis and
CC distinguishing between microbial and viral encephalitis. (I) is
CC applicable to a range of industries including the medical, agricultural
CC and industrial industries with specific uses including enviroprotection,
CC bioremediation, medical diagnosis, water quality control or food quality
CC control. (I) provides an ability to detect bacteria from samples which
CC are difficult to cultivate and that would in all practicality remain
CC undetected or under-estimated by viable culture count methods and enables
CC rapid differentiation of bacteria from viral infections within the
CC limited time constraints sometimes experienced in life-threatening
CC clinical situations. ABL59702 to ABL59821 represent 16S rDNA fragments,
CC and ABL59822 to ABL59830 represent primers and probes, used in the
CC exemplification of the present invention
XX
SQ Sequence 50 BP; 14 A; 12 C; 16 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 16 GCAAACAGGATTAGATACCC 35

RESULT 10
ABL59786
ID ABL59786 standard; DNA; 50 BP.
XX
AC ABL59786;
XX
DT 18-JUL-2002 (first entry)
XX
DE Campylobacter jejuni 16S rDNA fragment #3.
XX
KW Detection; microorganism; 16S rDNA; 16S rRNA; identification; gene;
KW microbial encephalitis; viral encephalitis; ds.
XX
OS Campylobacter jejuni.
XX
PN WO200210444-A1.
XX
PD 07-FEB-2002.
XX
PF 27-JUL-2001; 2001WO-AU000933.
XX
PR 28-JUL-2000; 2000AU-00009090.
XX
PA (UNSY) UNIV SYDNEY.
XX
PI Hunter N, Jacques NA, Martin FE, Nadkarni MA;

XX
DR WPI; 2002-404428/43.
XX
PT Polynucleotide useful as primer or probe for determining microbial
PT content in sample, has sequence which is comprised by 16S rDNA or 16S
PT rRNA, substantially conserved amongst two or more species of
PT microorganism.
XX
PS Example 12; Fig 1C; 101pp; English.
XX
CC The present invention describes a method for determining the total
CC microbial content in a sample, comprising amplifying a target nucleotide
CC sequence which is substantially conserved amongst 2 or more species of
CC microorganisms. Also describes is an isolated polynucleotide (I) or its
CC complement having a nucleotide sequence which is comprised by 16S rDNA or
CC 16S rRNA, substantially conserved amongst two or more species of
CC microorganism. (I) can be used: (1) as a primer or probe for determining
CC the total microbial content in a sample; (2) as a primer or probe for
CC identifying a microorganism by its genus in a sample; and (3) as a probe
CC for identifying a particular microorganism or prevalence of a particular
CC genus or species of microorganism, in a sample. (I) can also be used to
CC identify microorganisms at the genus or species level, and as a trap for
CC total microbial-derived target material; in assessing encephalitis and
CC distinguishing between microbial and viral encephalitis. (I) is
CC applicable to a range of industries including the medical, agricultural
CC and industrial industries with specific uses including enviroprotection,
CC bioremediation, medical diagnosis, water quality control or food quality
CC control. (I) provides an ability to detect bacteria from samples which
CC are difficult to cultivate and that would in all practicality remain
CC undetected or under-estimated by viable culture count methods and enables
CC rapid differentiation of bacteria from viral infections within the
CC limited time constraints sometimes experienced in life-threatening
CC clinical situations. ABL59702 to ABL59821 represent 16S rDNA fragments,
CC and ABL59822 to ABL59830 represent primers and probes, used in the
CC exemplification of the present invention
XX
SQ Sequence 50 BP; 14 A; 13 C; 16 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 16 GCAAACAGGATTAGATACCC 35

RESULT 11
ABL59805
ID ABL59805 standard; DNA; 50 BP.
XX
AC ABL59805;
XX
DT 18-JUL-2002 (first entry)
XX
DE Myxococcus xanthus 16S rDNA fragment #3.
XX
KW Detection; microorganism; 16S rDNA; 16S rRNA; identification; gene;
KW microbial encephalitis; viral encephalitis; ds.
XX
OS Myxococcus xanthus.
XX
PN WO200210444-A1.
XX
PD 07-FEB-2002.
XX
PF 27-JUL-2001; 2001WO-AU000933.
XX
PR 28-JUL-2000; 2000AU-00009090.
XX
PA (UNSY) UNIV SYDNEY.
XX
PI Hunter N, Jacques NA, Martin FE, Nadkarni MA;

XX
DR WPI; 2002-404428/43.
XX
PT Polynucleotide useful as primer or probe for determining microbial
PT content in sample, has sequence which is comprised by 16S rDNA or 16S
PT rRNA, substantially conserved amongst two or more species of
PT microorganism.
XX
PS Example 12; Fig 1C; 101pp; English.
XX
CC The present invention describes a method for determining the total
CC microbial content in a sample, comprising amplifying a target nucleotide
CC sequence which is substantially conserved amongst 2 or more species of
CC microorganisms. Also describes is an isolated polynucleotide (I) or its
CC complement having a nucleotide sequence which is comprised by 16S rDNA or
CC 16S rRNA, substantially conserved amongst two or more species of
CC microorganism. (I) can be used: (1) as a primer or probe for determining
CC the total microbial content in a sample; (2) as a primer or probe for
CC identifying a microorganism by its genus in a sample; and (3) as a probe
CC for identifying a particular microorganism or prevalence of a particular
CC genus or species of microorganism, in a sample. (I) can also be used to
CC identify microorganisms at the genus or species level, and as a trap for
CC total microbial-derived target material; in assessing encephalitis and
CC distinguishing between microbial and viral encephalitis. (I) is
CC applicable to a range of industries including the medical, agricultural
CC and industrial industries with specific uses including enviroprotection,
CC bioremediation, medical diagnosis, water quality control or food quality
CC control. (I) provides an ability to detect bacteria from samples which
CC are difficult to cultivate and that would in all practicality remain
CC undetected or under-estimated by viable culture count methods and enables
CC rapid differentiation of bacteria from viral infections within the
CC limited time constraints sometimes experienced in life-threatening
CC clinical situations. ABL59702 to ABL59821 represent 16S rDNA fragments,
CC and ABL59822 to ABL59830 represent primers and probes, used in the
CC exemplification of the present invention
XX
SQ Sequence 50 BP; 14 A; 13 C; 16 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 16 GCAAACAGGATTAGATACCC 35

RESULT 12
ABL59787
ID ABL59787 standard; DNA; 50 BP.
XX
AC ABL59787;
XX
DT 18-JUL-2002 (first entry)
XX
DE Helicobacter pylori 16S rDNA fragment #3.
XX
KW Detection; microorganism; 16S rDNA; 16S rRNA; identification; gene;
KW microbial encephalitis; viral encephalitis; ds.
XX
OS Helicobacter pylori.
XX
PN WO200210444-A1.
XX
PD 07-FEB-2002.
XX
PF 27-JUL-2001; 2001WO-AU000933.
XX
PR 28-JUL-2000; 2000AU-00009090.
XX
PA (UNSY) UNIV SYDNEY.
XX
PI Hunter N, Jacques NA, Martin FE, Nadkarni MA;

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XX
DR   WPI; 2002-404428/43.
XX
PT   Polynucleotide useful as primer or probe for determining microbial
PT   content in sample, has sequence which is comprised by 16S rDNA or 16S
PT   rRNA, substantially conserved amongst two or more species of
PT   microorganism.
XX
PS   Example 12; Fig 1C; 101pp; English.
XX
CC   The present invention describes a method for determining the total
CC   microbial content in a sample, comprising amplifying a target nucleotide
CC   sequence which is substantially conserved amongst 2 or more species of
CC   microorganisms. Also describes is an isolated polynucleotide (I) or its
CC   complement having a nucleotide sequence which is comprised by 16S rDNA or
CC   16S rRNA, substantially conserved amongst two or more species of
CC   microorganism. (I) can be used: (1) as a primer or probe for determining
CC   the total microbial content in a sample; (2) as a primer or probe for
CC   identifying a microorganism by its genus in a sample; and (3) as a probe
CC   for identifying a particular microorganism or prevalence of a particular
CC   genus or species of microorganism, in a sample. (I) can also be used to
CC   identify microorganisms at the genus or species level, and as a trap for
CC   total microbial-derived target material; in assessing encephalitis and
CC   distinguishing between microbial and viral encephalitis. (I) is
CC   applicable to a range of industries including the medical, agricultural
CC   and industrial industries with specific uses including enviroprotection,
CC   bioremediation, medical diagnosis, water quality control or food quality
CC   control. (I) provides an ability to detect bacteria from samples which
CC   are difficult to cultivate and that would in all practicality remain
CC   undetected or under-estimated by viable culture count methods and enables
CC   rapid differentiation of bacteria from viral infections within the
CC   limited time constraints sometimes experienced in life-threatening
CC   clinical situations. ABL59702 to ABL59821 represent 16S rDNA fragments,
CC   and ABL59822 to ABL59830 represent primers and probes, used in the
CC   exemplification of the present invention
XX
SQ   Sequence 50 BP; 14 A; 13 C; 16 G; 7 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 20;  DB 6;  Length 50;
  Best Local Similarity  100.0%;  Pred. No. 0.098;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         16 GCAAACAGGATTAGATACCC 35


RESULT 13
ABL59796
ID   ABL59796 standard; DNA; 50 BP.
XX
AC   ABL59796;
XX
DT   18-JUL-2002  (first entry)
XX
DE   Salmonella typhi 16S rDNA fragment #3.
XX
KW   Detection; microorganism; 16S rDNA; 16S rRNA; identification; gene;
KW   microbial encephalitis; viral encephalitis; ds.
XX
OS   Salmonella typhi.
XX
PN   WO200210444-A1.
XX
PD   07-FEB-2002.
XX
PF   27-JUL-2001; 2001WO-AU000933.
XX
PR   28-JUL-2000; 2000AU-00009090.
XX
PA   (UNSY ) UNIV SYDNEY.
XX
PI   Hunter N,  Jacques NA,  Martin FE,  Nadkarni MA;
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XX
DR   WPI; 2002-404428/43.
XX
PT   Polynucleotide useful as primer or probe for determining microbial
PT   content in sample, has sequence which is comprised by 16S rDNA or 16S
PT   rRNA, substantially conserved amongst two or more species of
PT   microorganism.
XX
PS   Example 12; Fig 1C; 101pp; English.
XX
CC   The present invention describes a method for determining the total
CC   microbial content in a sample, comprising amplifying a target nucleotide
CC   sequence which is substantially conserved amongst 2 or more species of
CC   microorganisms. Also describes is an isolated polynucleotide (I) or its
CC   complement having a nucleotide sequence which is comprised by 16S rDNA or
CC   16S rRNA, substantially conserved amongst two or more species of
CC   microorganism. (I) can be used: (1) as a primer or probe for determining
CC   the total microbial content in a sample; (2) as a primer or probe for
CC   identifying a microorganism by its genus in a sample; and (3) as a probe
CC   for identifying a particular microorganism or prevalence of a particular
CC   genus or species of microorganism, in a sample. (I) can also be used to
CC   identify microorganisms at the genus or species level, and as a trap for
CC   total microbial-derived target material; in assessing encephalitis and
CC   distinguishing between microbial and viral encephalitis. (I) is
CC   applicable to a range of industries including the medical, agricultural
CC   and industrial industries with specific uses including enviroprotection,
CC   bioremediation, medical diagnosis, water quality control or food quality
CC   control. (I) provides an ability to detect bacteria from samples which
CC   are difficult to cultivate and that would in all practicality remain
CC   undetected or under-estimated by viable culture count methods and enables
CC   rapid differentiation of bacteria from viral infections within the
CC   limited time constraints sometimes experienced in life-threatening
CC   clinical situations. ABL59702 to ABL59821 represent 16S rDNA fragments,
CC   and ABL59822 to ABL59830 represent primers and probes, used in the
CC   exemplification of the present invention
XX
SQ   Sequence 50 BP; 14 A; 12 C; 17 G; 7 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 20;  DB 6;  Length 50;
  Best Local Similarity  100.0%;  Pred. No. 0.098;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCAAACAGGATTAGATACCC 20
              ||||||||||||||||||||
Db         16 GCAAACAGGATTAGATACCC 35


RESULT 14
ABL59799
ID   ABL59799 standard; DNA; 50 BP.
XX
AC   ABL59799;
XX
DT   18-JUL-2002  (first entry)
XX
DE   Legionella pneumophila 16S rDNA fragment #3.
XX
KW   Detection; microorganism; 16S rDNA; 16S rRNA; identification; gene;
KW   microbial encephalitis; viral encephalitis; ds.
XX
OS   Legionella pneumophila.
XX
PN   WO200210444-A1.
XX
PD   07-FEB-2002.
XX
PF   27-JUL-2001; 2001WO-AU000933.
XX
PR   28-JUL-2000; 2000AU-00009090.
XX
PA   (UNSY ) UNIV SYDNEY.
XX
PI   Hunter N,  Jacques NA,  Martin FE,  Nadkarni MA;
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XX
DR WPI; 2002-404428/43.
XX
PT Polynucleotide useful as primer or probe for determining microbial
PT content in sample, has sequence which is comprised by 16S rDNA or 16S
PT rRNA, substantially conserved amongst two or more species of
PT microorganism.
XX
PS Example 12; Fig 1C; 101pp; English.
XX
CC The present invention describes a method for determining the total
CC microbial content in a sample, comprising amplifying a target nucleotide
CC sequence which is substantially conserved amongst 2 or more species of
CC microorganisms. Also describes is an isolated polynucleotide (I) or its
CC complement having a nucleotide sequence which is comprised by 16S rDNA or
CC 16S rRNA, substantially conserved amongst two or more species of
CC microorganism. (I) can be used: (1) as a primer or probe for determining
CC the total microbial content in a sample; (2) as a primer or probe for
CC identifying a microorganism by its genus in a sample; and (3) as a probe
CC for identifying a particular microorganism or prevalence of a particular
CC genus or species of microorganism, in a sample. (I) can also be used to
CC identify microorganisms at the genus or species level, and as a trap for
CC total microbial-derived target material; in assessing encephalitis and
CC distinguishing between microbial and viral encephalitis. (I) is
CC applicable to a range of industries including the medical, agricultural
CC and industrial industries with specific uses including enviroprotection,
CC bioremediation, medical diagnosis, water quality control or food quality
CC control. (I) provides an ability to detect bacteria from samples which
CC are difficult to cultivate and that would in all practicality remain
CC undetected or under-estimated by viable culture count methods and enables
CC rapid differentiation of bacteria from viral infections within the
CC limited time constraints sometimes experienced in life-threatening
CC clinical situations. ABL59702 to ABL59821 represent 16S rDNA fragments,
CC and ABL59822 to ABL59830 represent primers and probes, used in the
CC exemplification of the present invention
XX
SQ Sequence 50 BP; 15 A; 11 C; 16 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 16 GCAAACAGGATTAGATACCC 35

RESULT 15
ABL59801
ID ABL59801 standard; DNA; 50 BP.
XX
AC ABL59801;
XX
DT 18-JUL-2002 (first entry)
XX
DE Caulobacter vibrioides 16S rDNA fragment #3.
XX
KW Detection; microorganism; 16S rDNA; 16S rRNA; identification; gene;
KW microbial encephalitis; viral encephalitis; ds.
XX
OS Caulobacter vibrioides.
XX
PN WO200210444-A1.
XX
PD 07-FEB-2002.
XX
PF 27-JUL-2001; 2001WO-AU000933.
XX
PR 28-JUL-2000; 2000AU-00009090.
XX
PA (UNSY) UNIV SYDNEY.
XX
PI Hunter N, Jacques NA, Martin FE, Nadkarni MA;

XX
DR WPI; 2002-404428/43.
XX
PT Polynucleotide useful as primer or probe for determining microbial
PT content in sample, has sequence which is comprised by 16S rDNA or 16S
PT rRNA, substantially conserved amongst two or more species of
PT microorganism.
XX
PS Example 12; Fig 1C; 101pp; English.
XX
CC The present invention describes a method for determining the total
CC microbial content in a sample, comprising amplifying a target nucleotide
CC sequence which is substantially conserved amongst 2 or more species of
CC microorganisms. Also describes is an isolated polynucleotide (I) or its
CC complement having a nucleotide sequence which is comprised by 16S rDNA or
CC 16S rRNA, substantially conserved amongst two or more species of
CC microorganism. (I) can be used: (1) as a primer or probe for determining
CC the total microbial content in a sample; (2) as a primer or probe for
CC identifying a microorganism by its genus in a sample; and (3) as a probe
CC for identifying a particular microorganism or prevalence of a particular
CC genus or species of microorganism, in a sample. (I) can also be used to
CC identify microorganisms at the genus or species level, and as a trap for
CC total microbial-derived target material; in assessing encephalitis and
CC distinguishing between microbial and viral encephalitis. (I) is
CC applicable to a range of industries including the medical, agricultural
CC and industrial industries with specific uses including enviroprotection,
CC bioremediation, medical diagnosis, water quality control or food quality
CC control. (I) provides an ability to detect bacteria from samples which
CC are difficult to cultivate and that would in all practicality remain
CC undetected or under-estimated by viable culture count methods and enables
CC rapid differentiation of bacteria from viral infections within the
CC limited time constraints sometimes experienced in life-threatening
CC clinical situations. ABL59702 to ABL59821 represent 16S rDNA fragments,
CC and ABL59822 to ABL59830 represent primers and probes, used in the
CC exemplification of the present invention
XX
SQ Sequence 50 BP; 14 A; 12 C; 16 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAACAGGATTAGATACCC 20
||||||||||||||||||||
Db 16 GCAAACAGGATTAGATACCC 35

Search completed: August 4, 2004, 06:43:33
Job time : 166.337 secs